

AC Q9D1U4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days lactation, adult female mammary gland cDNA, RIKEN
DE full-length enriched library, clone:D730042M18 product:butyrophilin,
DE subfamily 1, member A1, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
EN [1]
EN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC MEDLINE=99279253; PubMed=10349636;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
EN [2]
EN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC MEDLINE=21085660; PubMed=11217851;
RX RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EN [3]
EN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC The FANTOM Consortium;
RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
EN [4]
EN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC MEDLINE=20499374; PubMed=11042159;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
EN [5]
EN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC MEDLINE=20530913; PubMed=11076861;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
EN [6]
EN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori P.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Segabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL ENBL; AK021333; BAB32377.1; -;
DR HSSP; Q63345; 1PKQ.

DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
SQ SEQUENCE 178 AA; 19816 MW; 06D3687AEDF80035 CRC64;

Query Match 8.8%; Score 90; DB 2; Length 178;
Best Local Similarity 33.1%; Pred. No. 4.7;
Matches 40; Conservative 15; Mismatches 40; Indels 26; Gaps 8;

QY 5 LLLIIMVHP--GSCALWVSQPP-IRTLGSSAFLPCSF--NAGQGLAIGSVTWFRD- 58
DB 13 LLLTLVLQPLTLD SAPFDVTA PQEPVLA LVGSDAELTCGFSFNASSEYM--ELLWFRQT 69
QY 59 -----EVPFGKVRNGTPEFRGLAPLASSRRLHDHQAELHIRDYRGHDASTYV 107
DB 70 RSTAVLLYRDGQEQEQQM-----TEYRGR-ATLATAGLL-DGRATLLIRDVRVSDQGEYR 123

QY 108 C 108
DB 124 C 124

Search completed: November 17, 2004, 00:19:30
Job time : 193 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2004, 00:02:14 ; Search time 152 seconds

(without alignments)
448.412 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAWMLLLILIMVHPGSCALW.....GTHCHSSDGGPRGVIPPEPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1364854

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Minimum DB seq length: 0
Maximum DB seq length: 190
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Post-processing: Minimum Match 0%.

Maximum Match 100%
Listing first 45 summaries

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Database :
1: Geneseq_23Sep04:
2: Genesexp1980s:
3: Genesexp1980s:
4: Genesexp2000s:
5: Genesexp2001s:
6: Genesexp2002s:
7: Genesexp2003as:
8: Genesexp2003bs:
9: Genesexp2004s:
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SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	1020	100.0	190	4	AA02769	Human NKp
2	1020	100.0	190	8	AD019810	Human PRO
3	1020	100.0	190	8	ADQ30923	Human NKp
4	1018	99.8	190	2	AAY06401	Human B-C
5	859	84.2	177	2	AAV06402	Human B-C
6	713	69.9	135	5	AAE19109	Human NKp
7	632	62.0	120	4	AAE02771	Human NKp
8	632	62.0	120	8	ADQ30924	Human NKp
9	204	20.0	33	4	AAE02773	Human NKp
10	204	20.0	33	8	ADQ30926	Human NKp
11	118.5	11.6	139	5	AAU75565	Murine T
12	106.5	10.4	138	4	AAW24182	Rhesus mo
13	106.5	10.4	151	7	ADD25748	Binding d
14	106	10.4	140	4	AAE68882	Human REC
15	104	10.2	174	3	AAE08208	Amino aci
16	103.5	10.1	136	4	ABJ11287	Human mem
17	103.5	10.1	161	4	AAE76011	Human col
18	103.5	10.1	187	2	AAE86945	Human T c
19	103.5	10.1	187	2	AAW97615	Human CTL
20	103.5	10.1	187	2	AAW97610	Human CTL
21	103.5	10.1	187	2	AAV41130	CTLA4 rec
22	102.5	10.0	152	3	AAE46464	Human S'
23	101.5	10.0	186	7	ADF74808	Human NOV
24	98	9.6	168	2	AAW42340	CTLA-4 ex
25	97	9.5	131	2	AAW22652	64-863 an

26	97	131	2	AAW19533	AAW19533	HSV 863 a
27	96.5	125	5	ABP52181	ABP52181	Human mon
28	96	18	4	AAE02770	AAE02770	Human NKp
29	95.5	129	5	ABG97832	ABG97832	Mouse 12E
30	95.5	129	5	ABG35333	ABG35333	Thrombopo
31	95.5	131	6	AAO29772	AAO29772	Rat myeli
32	95.5	130	2	AAW97817	AAW97817	Rat myeli
33	93.5	187	2	AAO29728	AAO29728	Soluble C
34	93	168	7	ADM05576	ADM05576	Human pro
35	92.5	142	6	ABR41570	ABR41570	Human DT
36	91.5	128	7	ADF65857	ADF65857	Murine T-
37	91.5	139	4	ABO27244	ABO27244	Human EXM
38	91	137	7	ADM07483	ADM07483	Canine im
39	91	167	7	ADM06106	ADM06106	Human pro
40	91	180	6	AAO050564	AAO050564	Novel hum
41	90.5	137	2	AAW70377	AAW70377	Anti-huma
42	90.5	147	4	AAK39507	AAK39507	Human pol
43	89.5	110	6	ABR55818	ABR55818	Lambda ch
44	89.5	114	8	ADH70114	ADH70114	Human vbe
45	89.5	121	2	AAV40837	AAV40837	SCA a rec

ALIGNMENTS

RESULT 1
AAE02769
ID AAE02769 standard: protein: 190 AA.

AC	AAE02769;
XX	
DT	06-AUG-2001 (first entry)
XX	
DE	Human Nkp30 receptor.
XX	
KW	Human; Nkp30 receptor; natural killer cell; cytostatic melanoma; hepatocarcinoma; lung adenocarcinoma; viral immunosuppressant; antiviral; drug; grafting enhancement therapy.
KW	
XX	
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	Peptide 1..18
FT	/label= Signal_peptide
FT	Protein 19..190
FT	/label= Mature_Nkp30_receptor_protein
FT	Region 19..138
FT	/label= Extracellular_region
FT	/note= "Forms an immunoglobulin (Ig)"
FT	42
FT	/note= "N-glycosylation site"
FT	Modified-site 121
FT	/note= "N-glycosylation site"
FT	Region 139..157
FT	/label= Transmembrane_region
FT	Region 158..190
FT	/label= Intracellular_region
XX	
PN	WO2001136630-A2.

15-NOV-2000: 2000WO-EP011697.

15-NOV-1999; 99CA-02288307.

15-NOV-1999; 99US-00440514.

(INNA-) INNATE PHARMA SAS.

(UYGE-) UNIV GENOVA.

Moretta A, Bottino C, Biassoni R;

XX

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DR WPI; 2001-329221/34.
DR N-PSDB; AAD06564.
XX
PT Novel compound, useful for detection and/or quantifying the presence of
PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.
XX
PS Claim 1; Fig 7B; 83pp; English.
XX
XX The invention relates to human Nkp30 receptor and its corresponding cDNA
XX molecule which is involved in natural cytotoxicity mediated by natural
XX killer (NK) cells and antibodies that identify the same. Nkp30 receptor
XX is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
XX expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
XX useful for detecting and/or quantifying the presence of NK cells in a
XX biological sample. The invention also provide kits for detecting and/or
XX quantifying the presence of NK cells, for the selective removal of NK
XX cells from a biological sample, for the positive and selective
XX purification of NK cells from a biological sample and for the in vitro
XX stimulation of NK cell cytotoxicity. The invention further provides a
XX pharmaceutical composition which is used as a drug for grafting
XX enhancement, graft versus host (GvH) inhibition, stimulation of graft
XX versus tumour (Gvt) and especially graft versus leukaemia (GvL), and for
XX the prevention, palliation and/or therapy of solid or liquid tumours,
XX such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
XX microorganism, notably viral infection. Nkp30 antibodies are useful for
XX identifying Nkp30 natural ligands and allow assessment of the level of
XX surface Nkp30 ligand expressed on an NK-susceptible target cell and the
XX comparison of this level to the standard physiological one. Hence Nkp30
XX antibodies are useful in the diagnosis of tumours or of infection. The
XX present sequence is human Nkp30 receptor
XX
SQ Sequence 190 AA;
Query Match 100.0%; Score 1020; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 8.3e-92;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMWLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEV 60
Db 1 MAMWLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
Qy 181 RGVIPERPCP 190
Db 181 RGVIPERPCP 190
RESULT 2
AD019810
ID AD019810 standard; protein; 190 AA.
XX
XX AD019810;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human PRO polypeptide #367.
XX
XX Human; PRO; immune related disorder; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
XX systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
XX autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
XX diabetes mellitus; renal disease; demyelinating disease;
XX central nervous system; peripheral nervous system;
XX demyelinating polyneuropathy; Guillain-Barre syndrome;
XX chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
FN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
XX WPI; 2004-420067/39.
XX
DR N-PSDB; ADO19809.
XX
XX Novel PRO polypeptide e.g., PRO89614, PRO71106, or PRO86388 useful for
XX treating an immune related disorder such as systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
XX spondyloarthritis.
XX
PS Claim 7; SEQ ID NO 734; 1731pp; English.
XX
XX The invention relates to human PRO polypeptides and the polynucleotides
XX encoding them. The polypeptides and polynucleotides are useful for
XX treating and diagnosing immune related disorders in mammals. The immune
XX related disorders include systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic
XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
XX haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
XX mellitus, immune-mediated renal disease, demyelinating diseases of the
XX central or peripheral nervous system, demyelinating polyneuropathy,
XX Guillain-Barre syndrome and chronic inflammatory demyelinating
XX polyneuropathy. This sequence represents a human PRO polypeptide of the
XX invention.
XX
SQ Sequence 190 AA;
Query Match 100.0%; Score 1020; DB 8; Length 190;
Best Local Similarity 100.0%; Pred. No. 8.3e-92;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMWLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEV 60
Db 1 MAMWLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
Qy 181 RGVIPERPCP 190
Db 181 RGVIPERPCP 190
RESULT 3
ADQ30923
ID ADQ30923 standard; protein; 190 AA.
XX
XX ADQ30923;
XX
XX 23-SEP-2004 (first entry)
XX
XX Human Nkp30 polypeptide.
XX
XX Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.
XX

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OS Homo sapiens.
XX Key Location/Qualifiers
XX Region 19..138
FT /label= Extracellular region
FT /note= "Region specifically described in Claim 3"
FT Region 20..133
FT /label
FT /note= "Immunogenic peptide specifically described in
FT Claim 3"
FT Region 139..157
FT /label= Transmembrane region
FT /note= "Region specifically described in Claim 3"
FT Region 158..190
FT /label= Cytoplasmic tail
FT /note= "Region specifically described in Claim 3"
XX WO2004056392-A1.
XX PN
XX PD
XX 08-JUL-2004.
XX 22-DEC-2003; 2003WO-EP014716.
XX 23-DEC-2002; 2002US-0435344P.
XX (INNA-) INNATE PHARMA.
XX Romagne F, Andre P;
PI
XX WPI; 2004-507595/48.
XX Pharmaceutical compositions that stimulate proliferation of natural
PT killer cells useful for therapy of melanoma, chronic myeloid, and
PT leukemia, comprise an anti-natural killer cell receptor antibody and
PT interleukins.
XX
PS Claim 3; SEQ ID NO 1; 35pp; English.
XX
XX The present sequence is that of human NKp30, a 190 amino acid polypeptide
CC (about 30 kDa on SDS-PAGE) that is selectively expressed by natural
CC killer (NK) cells, and particularly by mature NK cells. Claimed
CC pharmaceutical compositions that have a stimulating effect on the
CC proliferation of NK cells comprise an antibody such as an anti-NKp30
CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a
CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
CC antibody(ies) and cytokine(s) being administered together or separately
CC to a subject. The anti-NKp30 antibody is an isolated antibody or its
CC antigen-binding fragment which specifically binds to NKp30 or to a
CC fragment ADQ30924-ADQ30927 of NKp30. The pharmaceutical compositions,
CC when used for daily subcutaneous injection, comprising from 1 ng to 100
CC mg/kg (body weight) of antibody(ies), and lower than 1 million
CC units/square meters/day of cytokine(s), are useful for the prevention,
CC palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute
CC myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung
CC adenocarcinoma, neuroblastoma and for antimicrobial prevention,
CC palliation and therapy (claimed).
XX
SQ Sequence 190 AA;
Query Match 100.0%; Score 1020; DB 8; Length 190;
Best Local Similarity 100.0%; Pred. No. 8,3e-92;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMLLLLILMHPGSCALVWSQPPBIRTLGSSAFPLPCSFNAGSLAIGSVTFMFRDEV 60
DB 1 MAMLLLLILMHPGSCALVWSQPPBIRTLGSSAFPLPCSFNAGSLAIGSVTFMFRDEV 60
QY 61 VPKQEVNCTPFRGRPLASRFLHDQAEHLIRDVGRHDASIVVCVEVLGLGVGTG 120
DB 61 VPKQEVNCTPFRGRPLASRFLHDQAEHLIRDVGRHDASIVVCVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPQIGACTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180

Db 121 NGTRLVVEKEHPQIGACTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
QY 181 RGVIPERCP 190
DB 181 RGVIPERCP 190
RESULT 4
ID AAY06401 standard; protein; 190 AA.
AC AAY06401;
XX 20-SEP-1999 (first entry)
DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
KW signal transduction; immunomodulator; antiinflammatory;
KW autoimmune disease; inflammation; gene therapy; diagnosis.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..12
FT /note= "leader peptide"
FT Protein 13..190
FT /note= "mature protein"
FT Modified-site 42
FT /note= "N-glycosylated"
FT Modified-site 68
FT /note= "N-glycosylated"
FT Modified-site 121
FT /note= "N-glycosylated"
FT Domain 139..162
FT /note= "transmembrane domain"
FT Peptide 166..190
FT /note= "alternatively spliced C-terminal end"
XX WO9923867-A2.
XX 20-MAY-1999.
XX 05-NOV-1998; 98WO-US023826.
XX 07-NOV-1997; 97US-0064761P.
XX (BIOJ) BIOGEN INC.
XX Browning J;
XX WPI; 1999-418423/35.
XX N-PSDB; AAX59347.
XX Novel B-cell myelin oligodendrocyte glycoproteins.
XX Claim 2; Page 42; 43pp; English.
XX This sequence represents human BMOG, a novel member of the B cell myelin
CC oligodendrocyte glycoprotein family that is expressed by germinal centre
CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
CC identified. The protein is present primarily in the spleen, in lymph
CC nodes and in germinal centre B cells. It may have immunoregulatory
CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
CC regulate the immune system in autoimmune or inflammatory disease. Vectors
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
CC producing BMOG using these transformed host cells are also provided. BMOG
CC polypeptides can be used for modulating the immune system of a subject or
CC to inhibit signal transduction in a cell expressing BMOG by contacting it
CC with a soluble BMOG protein. The nucleic acid can be used for gene
CC therapy. The protein can also be used to target a toxin, imaging agent or
CC radionuclide to a cell expressing BMOG. (All claimed)
XX

SQ Sequence 190 AA;

Query Match 99.8%; Score 1018; DB 2; Length 190;
 Best Local Similarity 99.5%; Pred. No. 1.3e-91;
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWPRDEV 60
 DB 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWPRDEV 60

QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYVYQKCHMGTHCHSSDGP 180
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYVYQKCHMGTHCHSSDGP 180

QY 181 RGVIPERCP 190
 DB 181 RGVIPERCP 190

RESULT 5
 AAY06402
 ID AAY06402 standard; protein; 177 AA.
 AC AAY06402;
 DT 20-SEP-1999 (first entry)
 XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.
 KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
 KW signal transduction; immunomodulator; antiinflammatory;
 KW autoimmune disease; inflammation; gene therapy; diagnosis.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..12
 FT /note= "leader peptide"
 FT Protein 13..177
 FT /note= "mature protein"
 FT Modified-site 42
 FT /note= "N-glycosylated"
 FT Modified-site 68
 FT /note= "N-glycosylated"
 FT Modified-site 121
 FT /note= "N-glycosylated"
 FT Domain 139..162
 FT /note= "transmembrane domain"
 FT Peptide 165..177
 FT /note= "alternatively spliced C-terminal end"

XX WO923867-A2.
 XX 20-MAY-1999.
 XX 05-NOV-1998; 98WO-US023826.
 XX 07-NOV-1997; 97US-0064761P.
 XX (BIOJ) BIOGEN INC.
 XX Browning J;
 XX WPI; 1999-418423/35.
 DR N-PSDB; AAX59348.
 XX Novel B-cell myelin oligodendrocyte glycoproteins.
 XX Claim 2; Page 43; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 177 AA;

Query Match 84.2%; Score 859; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 4.9e-76;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWPRDEV 60

QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYVYQK 165
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYVYQK 165

RESULT 6
 AAE19109
 ID AAE19109 standard; protein; 135 AA.
 XX AAE19109;
 XX 21-MAY-2002 (first entry)
 XX Human Nkp30 protein.
 XX Human; natural killer cell activating protein; Nkp46; therapy; virucide;
 KW viral infection; natural killer cell; NK; Nkp44; imaging agent; cancer;
 KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; Nkp30.
 XX Homo sapiens.
 XX WO200208287-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-IL000664.
 XX 20-JUL-2000; 2000IL-00137419.
 XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX (UYNE) UNIV BEN-GURION NEGEV.
 XX Mandelboim O, Porgador A;
 XX WPI; 2002-195870/25.
 DR N-PSDB; RAD30466.
 XX New targeting complex capable of targeting an active substance to a target cell, comprising a target recognition segment and an active segment, useful for treating pathologies associated with viral infections or cancer.
 XX Example 1; Page 108; 113pp; English.

XX The invention relates to compositions and methods for the treatment and
CC detection of a variety of viral infections, by using complex agents
CC comprising the natural killer (NK) cells activating proteins, Nkp46 and
CC Nkp44 and functional fragments thereof, linked to therapeutic or imaging
CC agents. The complex is useful for treating pathologies associated with
CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein
CC -Barr virus, cytomegalovirus, vaccinia virus, ECV, MVM or herpes virus)
CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
CC the imaging and monitoring of cancer. The complex may also be used to
CC detect the presence of abnormal cells in a sample. The antibodies can be
CC used to qualitatively or quantitatively detect the ligand for the
CC complex. The present sequence is human Nkp30 protein
XX
SQ Sequence 135 AA;

Query Match 69.9%; Score 713; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 7.6e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMWLLILIMVHFGSCALWVSQPEIRTLGSSAFPLCSFNASQGRLAIGSVTWFRDEV 60
DB 1 MAMWLLILIMVHFGSCALWVSQPEIRTLGSSAFPLCSFNASQGRLAIGSVTWFRDEV 60

QY 61 VPGKEVRNGTPEPRGRPLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEPRGRPLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120

QY 121 NGTRLVVEKEHPQLG 135
DB 121 NGTRLVVEKEHPQLG 135

RESULT 7
AAE02771
ID AAE02771 standard; protein; 120 AA.
AC AAE02771;
XX
XX
DT 06-AUG-2001 (first entry)
XX
DE Human Nkp30 receptor extracellular region sequence.
XX
XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
KW therapy; extracellular region.
XX
OS Homo sapiens.
XX
XX WO200136630-A2.
XX
PD 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-EP011697.
XX
XX 15-NOV-1999; 99CA-02288307.
PR 15-NOV-1999; 99US-00440514.
XX
XX (INNA-) INNATE PHARMA SAS.
PA (UYGE-) UNIV GENOVA.
XX
XX Moretta A, Bottino C, Biassoni R;
XX
XX WPI; 2001-329221/34.
XX
XX Novel compound, useful for detection and/or quantifying the presence of
PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.
XX
XX Claim 1; Fig 7B; 83pp; English.
PS
XX
XX The invention relates to human Nkp30 receptor and its corresponding cDNA
CC molecule which is involved in natural cytotoxicity mediated by natural

CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor
CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
CC useful for detecting and/or quantifying the presence of NK cells in a
CC biological sample. The invention also provide kits for detecting and/or
CC quantifying the presence of NK cells, for the selective removal of NK
CC cells from a biological sample, for the positive and selective
CC purification of NK cells from a biological sample and for the in vitro
CC stimulation of NK cell cytotoxicity. The invention further provides a
CC pharmaceutical composition which is used as a drug for grafting
CC enhancement, graft versus host (GVH) inhibition, stimulation of graft
CC versus tumour (GVT) and especially graft versus leukaemia (GVL), and for
CC the prevention, palliation and/or therapy of solid or liquid tumours,
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
CC microorganism, notably viral infection. Nkp30 antibodies are useful for
CC identifying Nkp30 natural ligands and allow assessment of the level of
CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
CC comparison of this level to the standard physiological one. Hence Nkp30
CC antibodies are useful in the diagnosis of tumours or of infection. The
CC present sequence is the extracellular region of human Nkp30 receptor
XX
SQ Sequence 120 AA;

Query Match 62.0%; Score 632; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 5.9e-54;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LWVSQPEIRTLGSSAFPLCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78
DB 1 LWVSQPEIRTLGSSAFPLCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

QY 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNTRLVVEKEHPQLGAGT 138
DB 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNTRLVVEKEHPQLGAGT 120

RESULT 8
ADQ30924
ID ADQ30924 standard; protein; 120 AA.
XX
XX ADQ30924;
AC
XX
DT 23-SEP-2004 (first entry)
XX
DE Human Nkp30 extracellular region.
XX
KW Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.
XX
XX Homo sapiens.
OS
XX
XX WO2004056392-A1.
PN
XX
PD 08-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-EP014716.
PF
XX
XX 23-DEC-2002; 2002US-0435344P.
PR
XX
XX (INNA-) INNATE PHARMA.
PA
XX
XX Romagne F, Andre P;
PI
XX
XX WPI; 2004-507595/48.
DR
XX
XX Pharmaceutical compositions that stimulate proliferation of natural
PT killer cells useful for therapy of melanoma, chronic myeloid, and
PT leukemia, comprise an anti-natural killer cell receptor antibody and
PT interleukins.
XX
XX Claim 3; SEQ ID NO 2; 35pp; English.
PS
XX
XX The present sequence is that of the extracellular region of human Nkp30
CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by

CC natural killer (NK) cells, and particularly by mature NK cells. Claimed
 CC pharmaceutical compositions that have a stimulating effect on the
 CC proliferation of NK cells comprise an antibody such as an anti-NKp30
 CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
 CC antibody(ies) and cytokine(s) being administered together or separately
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its
 CC antigen-binding fragment which specifically binds to NKp30 or to a
 CC fragment, including the extracellular region, of NKp30. The
 CC pharmaceutical compositions, when used for daily subcutaneous injection,
 CC comprising from 1 mg to 100 mg/Kg (body weight) of antibody(ies), and
 CC lower than 1 million units/square meters/day of cytokine(s), are useful
 CC for the prevention, palliation and therapy of e.g. melanoma, chronic
 CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
 CC prevention, palliation and therapy (claimed).
 XX
 SQ Sequence 120 AA;

Query Match 62.0%; Score 632; DB 8; Length 120;
 Best Local Similarity 100.0%; Pred. No. 5.9e-54;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 LWSQPPEITLGGSSAFPCSNASQGRLAIGSVTFWDEVPVGGKVRNGTPEFRGRLA 78
 DB 1 LWSQPPEITLGGSSAFPCSNASQGRLAIGSVTFWDEVPVGGKVRNGTPEFRGRLA 60
 QY 79 PLASSRFLHDHQAELHTRDVRGHDASTYVCRVEVLGVLGVTGNGTRLVVEKEHPQLGAGT 138
 DB 61 PLASSRFLHDHQAELHTRDVRGHDASTYVCRVEVLGVLGVTGNGTRLVVEKEHPQLGAGT 120

RESULT 9
 AAEE02773
 ID AAEE02773 standard; peptide; 33 AA.
 XX
 AC AAEE02773;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE Human NKp30 receptor intracellular region sequence.
 XX
 KW Human, NKp30 receptor; natural killer cell; cytostatic; antimicrobial;
 KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
 KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
 KW therapy; intracellular region.
 XX
 OS Homo sapiens.
 XX
 PN WO200136630-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-EP011697.
 XX
 PR 15-NOV-1999; 99CA-02288307.
 PR 15-NOV-1999; 99US-00440514.
 XX
 XX (INNA-) INNATE PHARMA SAS.
 PA (UYGE-) UNIV GENOVA.
 XX
 PI Moretta A, Bottino C, Biassoni R;
 XX
 DR WPI; 2001-329221/34.
 XX

XX Novel compound, useful for detection and/or quantifying the presence of
 PT NK cells, comprises the amino acid sequences of the NKp30 molecule.
 XX
 PS Claim 1; Fig 7B; 83pp; English.
 XX
 CC The invention relates to human NKp30 receptor and its corresponding cDNA
 CC molecule which is involved in natural cytotoxicity mediated by natural
 CC killer (NK) cells and antibodies that identify the same. NKp30 receptor

CC is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively
 CC expressed on the surface of human mature NK cells. NKp30 and its cDNA are
 CC useful for detecting and/or quantifying the presence of NK cells in a
 CC biological sample. The invention also provide kits for detecting and/or
 CC quantifying the presence of NK cells, for the selective removal of NK
 CC cells from a biological sample, for the positive and selective
 CC purification of NK cells from a biological sample and for the in vitro
 CC stimulation of NK cell cytotoxicity. The invention further provides a
 CC pharmaceutical composition which is used as a drug for grafting
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft
 CC versus tumour (GVT) and especially graft versus leukaemia (GvL), and for
 CC the prevention, palliation and/or therapy of solid or liquid tumours,
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
 CC microorganism, notably viral infection. NKp30 antibodies are useful for
 CC identifying NKp30 natural ligands and allow assessment of the level of
 CC surface NKp30 ligand expressed on an NK-susceptible target cell and the
 CC comparison of this level to the standard physiological one. Hence NKp30
 CC antibodies are useful in the diagnosis of tumours or of infection. The
 CC present sequence is the intracellular region of human NKp30 receptor
 XX
 SQ Sequence 33 AA;

Query Match 20.0%; Score 204; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 158 STVYQKCHCHMGTHCHSSDGRGVIPPEPCP 190
 DB 1 STVYQKCHCHMGTHCHSSDGRGVIPPEPCP 33

RESULT 10
 ADQ30926
 ID ADQ30926 standard; protein; 33 AA.
 XX
 AC ADQ30926;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human NKp30 cytoplasmic tail.
 XX
 KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.
 XX
 OS Homo sapiens.
 XX
 PN WO2004056392-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-EP014716.
 XX
 PR 23-DEC-2002; 2002US-0435344P.
 XX
 PA (INNA-) INNATE PHARMA.
 XX
 PI Romagne F, Andre P;
 XX
 DR WPI; 2004-507595/48.
 XX
 PT Pharmaceutical compositions that stimulate proliferation of natural
 PT killer cells useful for therapy of melanoma, chronic myeloid, and
 PT leukemia, comprise an anti-natural killer cell receptor antibody and
 PT interleukins.
 XX
 PS Claim 3; SEQ ID NO 4; 35pp; English.

XX The present sequence is that of the cytoplasmic tail of human NKp30
 CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by
 CC natural killer (NK) cells, and particularly by mature NK cells. Claimed
 CC pharmaceutical compositions that have a stimulating effect on the
 CC proliferation of NK cells comprise an antibody such as an anti-NKp30
 CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the

CC antibody(ies) and cytokine(s) being administered together or separately
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its
 CC antigen-binding fragment which specifically binds to NKp30 or to a
 CC fragment, including the cytoplasmic tail, of NKp30. The pharmaceutical
 CC composition, when used for daily subcutaneous injection, comprising from
 CC 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1
 CC million units/square meters/day of cytokine(s), are useful for the
 CC prevention, palliation and therapy of e.g. melanoma, chronic myeloid
 CC leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
 CC prevention, palliation and therapy (claimed).

XX SQ Sequence 33 AA;

Query Match 20.0%; Score 204; DB 8; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e-12; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 STVYQKCHCHMGTHCHSSDGRGVIPRCP 190

|||||

Db 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

RESULT 11

AAU75565

ID AAU75565 standard; protein; 139 AA.

XX AC AAU75565;

XX XX 23-APR-2002 (first entry)

XX XX Murine T cell receptor beta chain.

XX XX Immunoglobulin superfamily; GP286; human; immunosuppressive;

XX KW autoimmune disease; rheumatoid arthritis; cancer; multiple sclerosis;

XX KW acquired immune deficiency syndrome; AIDS; inflammatory disorder;

XX KW pancreatitis; antirheumatic; antipsoriatic; dermatological; antianaemic;

XX KW cytostatic; antileukaemic; antiasthmatic; antiallergic;

XX KW T cell receptor beta chain.

XX MS Mus sp.

XX WO200200727-A2.

XX XX 03-JAN-2002.

XX XX 22-JUN-2001; 2001WO-US020038.

XX XX 23-JUN-2000; 2000US-0213630P.

XX XX 13-APR-2001; 2001US-0283813P.

XX XX (BIOJ) BIOGEN INC.

XX XX Carulli JP, Lukashin AV, Kilburn DR, Mathur P;

XX XX WPI; 2002-090520/12.

XX XX Isolated polynucleotide encoding a novel human immunoglobulin superfamily

XX XX member, named GP286, useful in the treatment of a disease condition that

XX XX relates to the immune system, e.g. a transplantation disorder or an

XX XX autoimmune disease.

XX XX Disclosure; Page 167; 180pp; English.

XX XX The invention relates to an isolated polynucleotide (I) encoding a novel

XX XX human immunoglobulin superfamily member, named GP286. The GP286

XX XX polynucleotide and polypeptide are useful for the treatment of a disease

XX XX condition that relates to the immune system, preferably a disease

XX XX condition that relates to T cells, e.g. a transplantation disorder, an

XX XX autoimmune disease (e.g. rheumatoid arthritis, systemic lupus

XX XX erythematosus, psoriasis, Sjogren's Syndrome, thyroiditis, Graves'

XX XX disease, pulmonary fibrosis, bronchiolitis obliterans, haemolytic anaemia

XX XX or Wegener's granulomatosis), cancer (e.g. leukaemia or lymphoma),

CC multiple sclerosis, graft versus host disease, Kawasaki syndrome,
 CC acquired immune deficiency syndrome (e.g. AIDS) or an inflammatory
 CC disorder (e.g. asthma, allergies, adult respiratory distress syndrome and
 CC acute pancreatitis or chronic pancreatitis). The gp286 nucleic acids can
 CC be used as probes for detecting, characterising and quantifying gp286
 CC nucleic acids. The present sequence represents the amino acid sequence of
 CC murine T cell receptor beta chain used in the method of the invention
 XX SQ Sequence 139 AA;

Query Match 11.6%; Score 118.5; DB 5; Length 139;

Best Local Similarity 30.2%; Pred. No. 0.0019;

Matches 39; Conservative 17; Mismatches 40; Indels 33; Gaps 7;

QY 20 WVS-----QPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWPRDE-----VVP 63

|||||

Db 18 WVSQDVQKQSPALSLEGTSSALRCNPS-----IATTVQWFLQNSRGSIMNLFYLP- 71

QY 64 KEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDAIYVCYRVEVLGLG--VGTGN 121

|||||

Db 72 ----GKKE-NGRLKSTFNSK---ESYSTLHIDAQLEDSTGYFCAAEVEGTGKLSFGK 122

QY 122 GTRLVVEKE 130

|||||

Db 123 GAKLTVSPD 131

RESULT 12

AAU24182

ID AAU24182 standard; protein; 138 AA.

XX AC AAU24182;

XX XX 12-OCT-2001 (first entry)

XX XX Rhesus monkey EST encoded protein SEQ ID NO: 1707.

XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

XX KW gene therapy; nutrition.

XX OS Macaca mulatta.

XX XX WO200154477-A2.

XX XX 02-AUG-2001.

XX XX 25-JAN-2001; 2001WO-US002687.

XX XX 25-JAN-2000; 2000US-00491404.

XX XX 17-JUL-2000; 2000US-00617746.

XX XX 03-AUG-2000; 2000US-00631451.

XX XX 15-SEP-2000; 2000US-00663870.

XX XX (HYSE-) HYSEQ INC.

XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX XX WPI; 2001-476164/51.

XX XX N-PSDB; AAH98841.

XX XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX XX antibodies and research use.

XX XX Claim 20; Page 1137-1138; 1275pp; English.

XX XX The present invention provides the protein and coding sequences of novel

XX XX proteins from a variety of organisms, including human, dog, cat, horse,

XX XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

XX XX urchin and tomato. These were derived from expressed sequence tags (ESTs)

XX XX from the organism of interest. They can be used in diagnostics,


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XX PD 01-FEB-2001.
XX PF 21-JUL-2000; 2000WO-US020035.
XX PR 21-JUL-1999; 99US-0145232P.
XX PR 07-OCT-1999; 99US-0158578P.
XX PR 12-NOV-1999; 99US-0165192P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Au-Young J, Bandman O, Tang YT, Yue H, Azimzai Y, Burford N;
XX PI Baughn MS, Lu DAM, Hillman JL, Patterson C, Lal P;
XX PR WPI; 2001-168554/17.
XX DR N-PSDB; AAF58606.
XX PT Novel receptors and associated proteins for diagnosis and treatment of
XX PT neurological disorders, immunological disorders including autoimmune/
XX PT inflammatory disorders and cell proliferative disorders such as cancer.
XX PS Claim 1; Page 104; 128pp; English.
XX CC The present sequence is a human RECAP (receptors and associated proteins)
XX CC polypeptide. RECAP polynucleotides and polypeptides are useful in the
XX CC diagnosis, treatment and prevention of neurological disorders such as
XX CC stroke, Alzheimer's disease, Pick's disease, Huntington's disease,
XX CC dementia, Parkinson's disease, Down's syndrome, amyotrophic lateral
XX CC sclerosis, multiple sclerosis, bacterial and viral meningitis, CJD
XX CC (Creutzfeldt-Jakob disease), GSS (Gerstmann-Strausler-Scheinker
XX CC syndrome), immunological disorders, including autoimmune/inflammatory
XX CC disorders such as AIDS, Digeorge's syndrome, severe combined
XX CC immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's
XX CC disease, Addison's disease, autoimmune thyroiditis, Crohn's disease,
XX CC diabetes mellitus, Good pasture's syndrome, gout, Grave's disease,
XX CC Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral,
XX CC bacterial, fungal, parasitic, protozoal, and helminthic infections; and
XX CC cell proliferation disorders such as arteriosclerosis, atherosclerosis,
XX CC cirrhosis, hepatitis and cancer
XX SQ Sequence 140 AA;
      Query Match 10.4%; Score 106; DB 4; Length 140;
      Best Local Similarity 29.2%; Pred. No. 0.033;
      Matches 40; Conservative 20; Mismatches 37; Indels 40; Gaps 9;
QY 17 CA---LW-----VSQPPE-INTLEGSSAFIPCSEFNASQGRLAIGSVTWFRDEVV 61
Db 7 CAFTVLQLGLWSGDEQVTSPEALRLQEGESSLNCSTVS---GLRGLFWYQD-- 60
QY 62 PGKEVRNGTPEFRGLAPLASSR-----FLDHQAEHLHIRDVRGHDASIYVCRVEVLG 114
Db 61 PGK-----GPEFLFTLYSAGEEKEKRLKATLTKKSEFLHTAPKPEDSASYLCAVQG-- 113
QY 115 LGVGT-----GNQTRLVV 127
Db 114 -GIGNVLHCGSGTQVVV 129
RESULT 15
ID AAB08208
XX AAB08208 standard; protein; 174 AA.
XX AC AAB08208;
XX DI 04-DEC-2000 (first entry)
XX DE Amino acid sequence of a rat shortened CTLA-4 polypeptide.
XX KW Shortened CTLA-4; sCTLA-4; lymphocyte cell surface receptor; B7; CTLA-4;
XX KW T cell response; B cell response; pathological condition.
XX OS Rattus norvegicus.

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XX Key Location/Qualifiers
XX PH 37..152
XX FT /note= "extracellular V domain"
XX FT Misc-difference 127
XX FT /note= "Tyr encoded by ACT"
XX FT Domain 153..174
XX FT /note= "cytoplasmic domain"
XX PN US6107056-A.
XX XX 22-AUG-2000.
XX PF 21-FEB-1997; 97US-00804180.
XX PR 22-FEB-1996; 96US-0012074P.
XX PA (OAKS/) OAKS M K.
XX PI Oaks MK;
XX DR WPI; 2000-578534/54.
XX DR N-PSDB; AAA63899.
XX PT Novel truncated CTLA-4 gene from human, rat and mouse useful for
XX PT regulating T cell and B cell responses in vivo for treating pathological
XX PT conditions.
XX PS Disclosure; Fig 2b; 22pp; English.
XX CC The present sequence represents a rat shortened CTLA-4 (sCTLA-4)
XX CC polypeptide. The polypeptide is a lymphocyte cell surface receptor for B7
XX CC molecules. The sCTLA-4 polypeptide lacks the entire membrane-spanning
XX CC domain of the classical CTLA-4 molecule. The sCTLA-4 nucleic acid
XX CC sequences are useful for producing the polypeptide. sCTLA-4 is useful for
XX CC regulating T cell and B cell response in vivo to treat pathological
XX CC conditions
XX SQ Sequence 174 AA;
      Query Match 10.2%; Score 104; DB 3; Length 174;
      Best Local Similarity 29.7%; Pred. No. 0.068;
      Matches 41; Conservative 23; Mismatches 56; Indels 18; Gaps 7;
QY 5 LLLILIMVHPGSCALWVSQPPPEITLEGSSAFIPC-----SFNASQGRLAIGSVTWFRDEV 60
Db 24 VLLSLFLPIFSEAIQVTPSVLASSHGVSFFCEYASSHTDEVRTVLQR--NDQV 81
QY 61 VPGKEVRNGTPEFRGLA---PLASSRFLDHQAEHLHIRDVRGHDASIYVCRVEVL--- 113
Db 82 T---EVCATTFTVKNLTGLFLDDPFCSGTF-NESRVNLTIGLRAADTGLYFCKVELMYPP 137
QY 114 GLGVGTGNGTRL-VVEKE 130
Db 138 PYFVGNGGTQIYVIAKE 155
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Job time : 155 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2004, 00:19:36 ; Search time 139 Seconds
(without alignments)
483.638 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAWMLLLILIMVHGPSALW.....GTHCHSDGPRGVIPEPCP 190

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Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 952392

Minimum DB seq length: 0

Maximum DB seq length: 190

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1020	100.0	190	13	US-10-036-444-2
2	1020	100.0	190	16	US-10-696-259-4
3	956.5	93.8	185	16	US-10-696-259-7
4	889.9	84.2	177	16	US-10-696-259-5
5	828.5	81.2	161	16	US-10-696-259-10
6	825	80.9	175	16	US-10-696-259-8
7	713	69.9	135	15	US-10-333-481-17
8	632	62.0	120	13	US-10-036-444-4
9	204	20.0	33	13	US-10-312-495-6
10	118.5	11.6	139	14	US-10-207-655-309
11	106.5	10.4	151	14	US-10-276-774-1657
12	103.5	10.1	136	15	US-10-106-698-6785
13	103.5	10.1	161	14	US-10-106-698-6785

14	103.5	10.1	187	17	US-10-732-847A-36	Sequence 36, Appl
15	101.5	10.0	186	15	US-10-383-201-22	Sequence 22, Appl
16	99.5	9.8	175	16	US-10-696-259-13	Sequence 13, Appl
17	99.5	9.8	186	17	US-10-748-112-2	Sequence 2, Appl
18	98	9.6	168	9	US-09-845-899A-7	Sequence 7, Appl
19	97	9.5	124	16	US-10-596-259-16	Sequence 16, Appl
20	96.5	9.5	125	15	US-10-432-006-2	Sequence 2, Appl
21	96	9.4	18	13	US-10-036-444-3	Sequence 3, Appl
22	95.5	9.4	129	15	US-10-399-518-141	Sequence 141, App
23	93.5	9.2	185	16	US-10-696-259-11	Sequence 11, Appl
24	93.5	9.2	187	10	US-09-014-761-1	Sequence 1, Appl
25	93.5	9.2	187	15	US-10-356-179-1	Sequence 1, Appl
26	93	9.1	168	15	US-10-108-260A-4261	Sequence 4261, Ap
27	92	9.0	175	16	US-10-596-259-12	Sequence 12, Appl
28	91	8.9	139	16	US-10-327-598-1078	Sequence 1078, Ap
29	91	8.9	167	15	US-10-108-260A-4791	Sequence 4791, Ap
30	91	8.9	187	14	US-10-243-552-572	Sequence 572, Appl
31	89.5	8.8	110	14	US-10-369-805-50	Sequence 50, Appl
32	89.5	8.8	114	9	US-09-263-959-308	Sequence 308, App
33	89.5	8.8	124	14	US-10-207-655-314	Sequence 314, App
34	89	8.7	162	15	US-10-424-599-176578	Sequence 176578, Sequence 73, Appl
35	88.5	8.7	162	15	US-10-364-743-73	Sequence 5, Appl
36	88	8.6	19	13	US-10-036-444-5	Sequence 39, Appl
37	88	8.6	127	15	US-10-452-646-39	Sequence 6, Appl
38	88	8.6	156	14	US-10-320-352-6	Sequence 32704, A
39	87.5	8.6	115	14	US-10-029-386-32704	Sequence 1112, Ap
40	87	8.5	131	16	US-10-327-598-1112	Sequence 44, Appl
41	85.5	8.4	109	14	US-10-001-934-44	Sequence 75, Appl
42	85.5	8.4	109	15	US-10-275-046-75	Sequence 81, Appl
43	85.5	8.4	120	9	US-09-910-059-81	Sequence 4, Appl
44	85.5	8.4	125	16	US-10-432-006-4	Sequence 74, Appl
45	84.5	8.3	108	10	US-09-791-153A-74	

ALIGNMENTS

RESULT 1

US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1 triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036.444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell

Query Match 100.0%; Score 1020; DB 13; Length 190;

Best Local Similarity 100.0%; Pred. No. 3,le-93;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWMLLLILIMVHGPSALWVSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEV 60

DB 1 MAWMLLLILIMVHGPSALWVSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEV 60

QY 61 VPGKEVNGTPEFGRLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120

DB 61 VPGKEVNGTPEFGRLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 121 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYYQK 165

RESULT 5

US-10-696-259-10

Query Match 81.2%; Score 828.5; DB 16; Length 161;

Best Local Similarity 99.4%; Pred. No. 2.9e-74;

Matches 161; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 119

QY 121 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYY 162

Db 120 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYY 161

RESULT 6

US-10-696-259-8

Query Match 81.2%; Score 828.5; DB 16; Length 161;

Best Local Similarity 99.4%; Pred. No. 2.9e-74;

Matches 161; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 119

QY 121 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYY 162

Db 120 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYY 161

RESULT 7

US-10-333-481-17

Query Match 80.9%; Score 825; DB 16; Length 175;

Best Local Similarity 98.2%; Pred. No. 7.2e-74;

Matches 162; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 59

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 60 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 118

QY 121 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYYQK 165

Db 119 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYYHCK 163

RESULT 8

US-10-036-444-4

Query Match 69.9%; Score 713; DB 15; Length 135;

Best Local Similarity 100.8%; Pred. No. 7.3e-63;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVVEKEHPQLG 135

Db 121 NGTRLVVEKEHPQLG 135

RESULT 8

US-10-036-444-4

Query Match 69.9%; Score 713; DB 15; Length 135;

Best Local Similarity 100.8%; Pred. No. 7.3e-63;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVVEKEHPQLG 135

Db 121 NGTRLVVEKEHPQLG 135

US-10-696-259-8

Query Match 80.9%; Score 825; DB 16; Length 175;

Best Local Similarity 98.2%; Pred. No. 7.2e-74;

Matches 162; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 59

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 60 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 118

QY 121 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYYQK 165

Db 119 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYYHCK 163

RESULT 7

US-10-333-481-17

Query Match 80.9%; Score 825; DB 16; Length 175;

Best Local Similarity 98.2%; Pred. No. 7.2e-74;

Matches 162; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 59

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 60 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 118

QY 121 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYYQK 165

Db 119 NGTRLVVEKEHPQLGAGTIVLLLRAGFYAVSFSLVAVGSTVYYHCK 163

RESULT 8

US-10-036-444-4

Query Match 69.9%; Score 713; DB 15; Length 135;

Best Local Similarity 100.8%; Pred. No. 7.3e-63;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVVEKEHPQLG 135

Db 121 NGTRLVVEKEHPQLG 135

RESULT 8

US-10-036-444-4

Query Match 69.9%; Score 713; DB 15; Length 135;

Best Local Similarity 100.8%; Pred. No. 7.3e-63;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWRDEV 60

QY 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG 120

QY 121 NGTRLVVEKEHPQLG 135

Db 121 NGTRLVVEKEHPQLG 135

; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-4

Query Match 62.0%; Score 632; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.3e-55;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 19 LWSVQPEIRTLGSSAFPCSFNASQGRLAIGSVTFWFRDEVPVPGKEVRNGTPEFRGLA 78
Db 1 LWSVQPEIRTLGSSAFPCSFNASQGRLAIGSVTFWFRDEVPVPGKEVRNGTPEFRGLA 60
Qy 79 PLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTNGTRLVVEKEHPOLGAGT 138
Db 61 PLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTNGTRLVVEKEHPOLGAGT 120

RESULT 9
US-10-036-444-6
; Sequence 6, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-6

Query Match 20.0%; Score 204; DB 13; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 158 STVYQKCHCHMGTHCHSSDGRGVIPRCP 190
Db 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

RESULT 10
US-10-312-495-6
; Sequence 6, Application US/10312495
; Publication No. US20030165495A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: A099CT000454-124
; CURRENT APPLICATION NUMBER: US/10/312,495
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/213,630
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/283,813
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6

; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-312-495-6

Query Match 11.6%; Score 118.5; DB 14; Length 139;
Best Local Similarity 30.2%; Pred. No. 0.0011;
Matches 39; Conservative 17; Mismatches 40; Indels 33; Gaps 7;
Qy 20 WVS-----OPPRTLEGSSAFPCSFNASQGRLAIGSVTFWFRDE-----VWPG 63
Db 18 WVSQDQVKQSPSALSQEGTSSALRCNFS-----IATTIVQWFLQNSRSLXNLFVLP- 71
Qy 64 KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLG- -VGTGN 121
Db 72 -----GTKE-NGRLKSTFNSK---ESYSTLHIRDAQLEDSDGTVFCAAEVEGTGSKLSFGK 122
Qy 122 GTRLVVEKE 130
Db 123 GAKLTVSPD 131

RESULT 11
US-10-207-655-309
; Sequence 309, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390089.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 309
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-309

Query Match 10.4%; Score 106.5; DB 14; Length 151;
Best Local Similarity 28.0%; Pred. No. 0.02; Mismatches 20; Indels 21; Gaps 5;
Matches 40; Conservative 20; Mismatches 62; Indels 21; Gaps 5;
Qy 4 MLLILIMVHP--GSCALWVSQPEIRTLGSSAFPCSFNASQGRLAIGSVTFWFRDEV 61
Db 10 LLSLVALLFPMSMASMAHVQAQPAVLASSRGIASFVCEY-ASPGKATEVRVTVLROADS 68
Qy 62 PKQEVNRGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEV 112
Db 69 QVTECAATYMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGYICKVEL 122
Qy 113 L---GLGVGTNGTRLVVEKEHP 132
Db 123 MYPPYVLGNGTQIYVIDPEP 145

RESULT 12
US-10-276-774-1657
; Sequence 1657, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27

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; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1657
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1657

Query Match
Best Local Similarity 10.1%; Score 103.5; DB 15; Length 136;
Matches 29; Conservative 11; Mismatches 37; Indels 27; Gaps 3;

QY 15 GSCALWVQBP-----PEIRTEGSSAFPLPCSFNASQGLAIGSVTWFRDEVVPGKEVR 67
Db 15 GKRLVVQVPEVLENGLDLSTTGSHAFPLCKARGSP-----PNITWDKD----- 61
QY 68 NGTPEPRGLAPLASSRFLHDQAEHLHIRDVRGHDASIYVCRVE 111
Db 62 -----GQPVSAEGKFTIQPSGELLVKNLEQDAGTYTCTAE 98

RESULT 13
US-10-106-698-6785
; Sequence 6785, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PAC05P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patent In Ver. 3.0
; SEQ ID NO 6785
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6785

Query Match
Best Local Similarity 10.1%; Score 103.5; DB 14; Length 161;
Matches 43; Conservative 26; Mismatches 65; Indels 27; Gaps 9;

QY 1 MAWMLLLILIMVH-PGSCALW-VSQPPEIRTEGSSAFPLPCSFNASQGLAIGSVTWFRD 58
Db 3 MAWAPLLLTLLAHTCTGSAIFMLTQPHSVSEPGKTVTISCT--RSSGSIASNYVQWFOQ 60
QY 59 EVVPG-----KEVRNGTPE-PRGLAPLASSRFLHDQAEHLHIRDVRGHDASIYV 107
Db 61 R-PGSSPTTVIVEDNQPSGVDFRFGSIDSSNS-----ASITISGLKTEADYY 111
QY 108 CRVEVLGLVGVTGNGTRLVV--EKEHPQLGAGTVLLLRAGF 146
Db 112 CQ-SYDSSNVVFGGKTKLTVLQAQGLPLGHSVPALLXSF 151

RESULT 14
US-10-732-847A-36
; Sequence 36, Application US/10732847A
; Publication No. US20040202650A1
; GENERAL INFORMATION:
```

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; APPLICANT: GRIBBEN, JOHN G.
; APPLICANT: FREEMAN, GORDON J.
; APPLICANT: NADLER, LEE M.
; APPLICANT: RENNERT, PAUL
; APPLICANT: JELLIS, CINDY L.
; APPLICANT: GREENFIELD, EDWARD
; APPLICANT: GRAY, GARY S.
; TITLE OF INVENTION: METHODS OF INHIBITING T CELL
; TITLE OF INVENTION: PROLIFERATION OR IL-2 ACCUMULATION WITH CTLA-4
; FILE REFERENCE: RPI-016CPA2DV
; CURRENT APPLICATION NUMBER: US/10/732,847A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 08/253783
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein
US-10-732-847A-36

Query Match
Best Local Similarity 10.1%; Score 103.5; DB 17; Length 187;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTEGSSAFPLPCSFNASQGLAIGSVTWFRDEVVPGKEVRNGTPEFRGL 77
Db 1 AMHVAQPAVVLASSRSGTASFVQY-ASFGKATEVTVTLRQADSQVTEVCATYMGNEL 59
QY 78 APLASSRFLHD-----HQAEHLHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDISICTGTSSGNQVNLTIQGLRAMDTGLYCKVELMYPYVYLIGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA---GFIYAVSFSLVAV 156
Db 114 YVIDPECPDSDFLLWTLAIVSSGLFFYSFLLTAV 148

RESULT 15
US-10-383-201-22
; Sequence 22, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
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; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 22
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-22

Query Match      10.0%; Score 101.5; DB 15; Length 186;
Best Local Similarity 26.1%; Pred. No. 0.08;
Matches 41; Conservative 20; Mismatches 65; Indels 31; Gaps 6;

Qy 6 LLLIIMVHPGSC-ALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGK 64
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 24 LLFFLLFIPVECKAMHVAQFALVLAASSRGIAFVCEY-ASPGKATEVRVTVLRQADSQVT 82
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 65 EVRNGTPEFRGRPLAPLASSRFLHD-----HQAELHIRDVVRGHDAIYVCRVEVL-- 113
   |||||::||::||::||::||::||::||::||::||::||::||::||::||::||::
Db 83 EVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRANDTGLYICKVELMYP 136
   |||||::||::||::||::||::||::||::||::||::||::||::||::||::||::
Qy 114 ---GLGVGTGNGTRLVVEKEHPOLGAGTVLLLRAGFY 147
   |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 137 PPVYLGIGNGTQIYVILKKRSP-----LTTGVY 164
   |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
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Search completed: November 17, 2004, 00:31:36
Job time : 140 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 00:11:05 ; Search time 39 Seconds
(without alignments)
323.088 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAWMLLLILIMVHPGSCALW.....GTHCHSSDGRGVIPEPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 367650

Minimum DB seq length: 0

Maximum DB seq length: 190

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	10.2	174	3	US-08-804-180C-4
2	103.5	10.1	187	1	US-08-067-684-14
3	103.5	10.1	187	1	US-08-008-898-14
4	103.5	10.1	187	1	US-08-459-818-14
5	103.5	10.1	187	2	US-08-889-666-14
6	103.5	10.1	187	2	US-08-465-078-14
7	103.5	10.1	187	2	US-08-725-776-14
8	103.5	10.1	187	2	US-08-488-062-14
9	103.5	10.1	187	3	US-08-228-208A-14
10	103.5	10.1	187	4	US-08-253-783-36
11	103.5	10.1	187	5	PCT-US95-06726-36
12	97	9.5	131	1	US-08-305-683A-4
13	89.5	8.8	120	3	US-08-171-945-89
14	89.5	8.8	137	3	US-08-804-180C-2
15	87.5	8.6	120	4	US-09-472-087-102
16	85.5	8.4	120	3	US-09-171-945-81
17	84	8.2	121	1	US-08-388-672A-20
18	84	8.2	126	3	US-09-080-554-20
19	83.5	8.2	120	3	US-09-171-945-79
20	83.5	8.2	120	3	US-08-171-945-91
21	82.5	8.1	124	3	US-08-630-172-4
22	82.5	8.1	124	3	US-09-375-419-4
23	82	8.0	135	2	US-08-470-139-28
24	82	8.0	135	3	US-09-347-061-28
25	82	8.0	135	4	US-09-855-271-28
26	82	8.0	159	3	US-08-430-503-36
27	81.5	8.0	92	3	US-08-328-383B-15

Sequence 26, Appl
Sequence 4, Appli
Sequence 110, App
Sequence 110, App
Sequence 4, Appli
Sequence 4389, Ap
Sequence 60065, A
Sequence 40, Appl
Sequence 31, Appl
Sequence 24, Appl
Sequence 34, Appl
Sequence 5, Appli
Sequence 4, Appli
Sequence 38, Appl
Sequence 34, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 34849, A

28 81.5 8.0 110 2 US-08-362-780-26
29 81.5 8.0 111 4 US-09-424-840-4
30 81.5 8.0 128 1 US-08-476-039-110
31 81.5 8.0 128 1 US-08-476-349A-110
32 81.5 8.0 128 3 US-08-523-894-4
33 81.5 8.0 136 4 US-09-513-999C-4389
34 81.5 8.0 175 4 US-09-270-767-60065
35 81 7.9 159 3 US-09-430-503-40
36 80 7.8 114 4 US-08-055-006-31
37 80 7.8 122 4 US-09-424-840-24
38 80 7.8 159 3 US-09-430-503-34
39 79.5 7.8 109 3 US-09-157-370-5
40 79 7.7 132 2 US-08-345-321-4
41 79 7.7 159 3 US-09-430-503-38
42 77.5 7.6 109 3 US-09-460-384-34
43 77.5 7.6 131 3 US-08-836-561-25
44 77.5 7.6 131 4 US-08-434-122-25
45 77.5 7.6 138 4 US-09-270-767-34849

ALIGNMENTS

RESULT 1
US-08-804-180C-4
; Sequence 4, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: Polypeptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: Internal fragment
; ORIGINAL SOURCE:
; ORGANISM: Rattus No. 6107056vegicus
; STRAIN: ACI
; DEVELOPMENTAL STAGE: Adult
; CELL TYPE: Splenocyte
; FEATURE:
; NAME/KEY: Rat sCTLA-4
; IDENTIFICATION METHOD: Found by experiment
; OTHER INFORMATION: E7 binding protein

US-08-804-180C-4


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-078-14

- Query Match
  Best Local Similarity 10.1%; Score 103.5; DB 2; Length 187;
  Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPPEIRTELGSSAFIPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEPRGRL 77
Db 1 AMHVAQPAVVILASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVTEVCAATYMMGNEL 59
QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA---GFYAVSFLSVAV 156
Db 114 YVIDPEPCPSDFLLWILAAVSSGLFFYSFLLTAV 148

RESULT 7
US-08-725-776-14
; Sequence 14, Application US/08725776
; Patent No. 5968510
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dame, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kienner, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 18-JAN-1995
; APPLICATION NUMBER: US/08/725,776
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
```

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-725-776-14

Query Match
  Best Local Similarity 10.1%; Score 103.5; DB 2; Length 187;
  Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPPEIRTELGSSAFIPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEPRGRL 77
Db 1 AMHVAQPAVVILASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVTEVCAATYMMGNEL 59
QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA---GFYAVSFLSVAV 156
Db 114 YVIDPEPCPSDFLLWILAAVSSGLFFYSFLLTAV 148

RESULT 8
US-08-488-062-14
; Sequence 14, Application US/08488062
; Patent No. 5977318
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dame, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kienner, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/488,062
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-062-14

Query Match
  Best Local Similarity 10.1%; Score 103.5; DB 2; Length 187;
  Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;
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Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTELGSSAFPCSFNASQRLAIGSVTFWFRDEVVPGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVLASSRGIAFVCEY-ASPGKATEVRVTVLRQADSQVTEVCAATYMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113

QY 126 VVEKEHPQAGTVLLRA-----GFYAVSFLSVAV 156
Db 114 YVIDPEPCPSDFLLWILAASVSSGLFFYSFLLTAV 148

RESULT 9
US-08-228-208A-14
; Sequence 14, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dandle, Nalin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-208A-14

Query Match 10.1%; Score 103.5; DB 3; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTELGSSAFPCSFNASQRLAIGSVTFWFRDEVVPGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVLASSRGIAFVCEY-ASPGKATEVRVTVLRQADSQVTEVCAATYMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113

QY 126 VVEKEHPQAGTVLLRA-----GFYAVSFLSVAV 156
Db 114 YVIDPEPCPSDFLLWILAASVSSGLFFYSFLLTAV 148

RESULT 10
US-08-253-783-36
; Sequence 36, Application US/08253783
; Patent No. 6719972
; GENERAL INFORMATION:
; APPLICANT: John G. Gribben, Gordon J. Freeman, Lee M. Nadler, Paul
; TITLE OF INVENTION: Ligands for Induction of Antigen Specific
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,783
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-253-783-36

Query Match 10.1%; Score 103.5; DB 4; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRTELGSSAFPCSFNASQRLAIGSVTFWFRDEVVPGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVLASSRGIAFVCEY-ASPGKATEVRVTVLRQADSQVTEVCAATYMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113

QY 126 VVEKEHPQAGTVLLRA-----GFYAVSFLSVAV 156
Db 114 YVIDPEPCPSDFLLWILAASVSSGLFFYSFLLTAV 148

RESULT 11
PCT-US95-06726-36
; Sequence 36, Application PC/TUS9506726
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Ligands for Induction of Antigen Specific
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; APOPTOSIS IN

```

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06726
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,783
; FILING DATE: 03 JUNE 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-016PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-06726-36

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Query Match 10.1%; Score 103.5; DB 5; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSOPPEIRTLGSSAFPCFNASQGRLAIGSVTWFRDEVPQKEVNGTPEFRGL 77
DQ 1 AMHVAQPAVVLASSRGIASFVQY-ASPGKATEVTVTLRQADSQVTECAATYMGNEL 59
QY 78 APLASSRFLHD-----HQELHIRDVRGHDAIYVCRVEVL---CLGVGTGNGTRL 125
DQ 60 T-----FLDSDICTGTSGNQNLTIQGLRAMDTGLYICKVELMYPYPYILGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAV 156
DQ 114 YVIDPECPDSDFLMLLAWSGLFFYSFLLTAV 148

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RESULT 12
US-08-305-683A-4
; Sequence 4, Application US/08305683A
; Patent No. 5646041
; GENERAL INFORMATION:
; APPLICANT: HAREFELDT, Elisabeth
; APPLICANT: LAKE, Philip
; APPLICANT: NOTTAGE, Barbara
; APPLICANT: OSTBERG, Lars G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,683A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,279
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-005230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-305-683A-4

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Query Match 9.5%; Score 97; DB 1; Length 131;
Best Local Similarity 28.2%; Pred. No. 0.011;
Matches 40; Conservative 22; Mismatches 52; Indels 28; Gaps 9;

QY 1 MAWMLLLILIMVH-PGSCALWV-SQPPEIRTLGSSAFPCFNASQGRLAIG-SVTWFR 57
DQ 1 MAWSPLLLTLLAHCTGSAQSVLTQPPSVGAPGQGVTLST--GSRNIGAGYDVHWYQ 58
QY 58 DEVVPGKEVR-----NGTPE-PRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIY 106
DQ 59 H-LPGTAPKLLIYDNNRSGVDFRSGSKSGTSAS-----LAITGLQAEDEADY 107
QY 107 VCRVEVLGL-GVGTGNGTRLW 127
DQ 108 YCQSYDGLSGSIFGGGKTLTV 129

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RESULT 13
US-09-171-945-89
; Sequence 89, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-89

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Query Match 8.8%; Score 89.5; DB 3; Length 120;
Best Local Similarity 27.8%; Pred. No. 0.065;
Matches 32; Conservative 10; Mismatches 34; Indels 39; Gaps 6;

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QY 20 WVSQPEIRTEGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG-----TPFERG 75
Db 36 WVRQPF-----GR-GLGWIGWIDPE-----NGDTEYAPKFRG 66
QY 76 RLAPLASSRFLHDOAELHIRDVRGHDSIYVCRVEVLGLGVGT---GNGTRLVV 127
Db 67 RAYMLADS---SKNQASLRSLSSVTAADTAVYVCHVLIYAGYLANDYWGQGLTVV 118

RESULT 14
US-08-804-180C-2
; Sequence 2, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: scTLA-4 and its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: no
; HYPOTHETICAL: no
; FRAGMENT TYPE: Mature Polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapien
; DEVELOPMENTAL STAGE: Adult
; TISSUE TYPE: Lymphnode
; FEATURE:
; NAME/KEY: Human scTLA-4
; IDENTIFICATION METHOD: Found by experiment
; OTHER INFORMATION: Asn 76 and Asn 108 represent N-linked glycosylation; B7 binds
US-08-804-180C-2

Query Match 8.8%; Score 89.5; DB 3; Length 137;
Best Local Similarity 25.2%; Pred. No. 0.078;
Matches 33; Conservative 18; Mismatches 59; Indels 21; Gaps 4;
QY 21 VSQPPEIRTEGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPFERGLAPL 80
Db 3 VAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNELT-- 59
QY 81 ASSRFLHD-----HQAEIHIRDVRGHDSIYVCRVEVL-----GLGVGTGNGTRLV 126
Db 60 ----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQIYVI 115
QY 127 VEKEHPQLGAG 137

Db 116 AKKKPSYNRG 126
RESULT 15
US-09-472-087-102
; Sequence 102, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 102
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-102
Query Match 8.6%; Score 87.5; DB 4; Length 120;
Best Local Similarity 27.4%; Pred. No. 0.11;
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;
QY 21 VSQPPEIRTEGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPFERGLAPL 80
Db 3 VAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNELT-- 59
QY 81 ASSRFLHD-----HQAEIHIRDVRGHDSIYVCRVEVL-----GLGVGTGNGTRLV 128
Db 60 ----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQIYVI 115
QY 129 KEHP 132
Db 116 DPEP 119
Search completed: November 17, 2004, 00:20:58
Job time : 40 secs

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Db      3 VROSPQSLTWEGETAINGSYEDS-----TFDYFPWYR--LFPGE-----SPALLIAIRP 51
Qy      62 LAS-----SRFL-----HDHQAELHIRDVRGHDAIYVCRVEVLG--GVGTNGTGLVV 109
Db      52 VSNKXEDGRFTIFNKRKKLSLHIDSQCDSATFCAARSTGFASALTFFGSGTRVIV 110

RESULT 7
JH0342
T-cell receptor alpha chain V region (PID3A6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: JH0342
R:Taylor, A.H.; Haberman, A.M.; Gerhard, W.; Caton, A.J.
J. Exp. Med. 172, 1643-1651, 1990
A:Title: Structure-function relationships among highly diverse T cells that recognize a
A:Reference number: JH0333; MUID:91079767; PMID:1701821
A:Accession: JH0342
A:Molecule type: mRNA
A:Residues: 1-108 <RAY>
A:Cross-references: GB:M34212; NID:G201185; PIDN:AAA58756.1; PID:G201186
C:Comment: This T-cell receptor recognizes a determinant from influenza virus hemagglutinin
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: receptor; T-cell
F:15-88/Domain: immunoglobulin homology <IMM>

Query Match      13.8%; Score 87; DB 2; Length 108;
Best Local Similarity 31.0%; Pred. No. 0.13;
Matches 35; Conservative 16; Mismatches 36; Indels 26; Gaps 8;

Qy      3 VSOPPEIRTI-EGSSAFPCSFNASQGRLAIGSVTWFR--RDEVVPGKEVR-----NGTPE 54
Db      3 VQSPASLVQEGENAEIQCNFST-----LNSQWFFYORPE---GSLVSLFYNPGTKQ 54

Qy      55 FRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLG-----LGVTG 101
Db      55 -SGR---LTSTTVIKERRSSLHSSQITDSGYLCAVEATGNNKLTGQGT 103

RESULT 8
G30603
T-cell receptor alpha chain V region (C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 23-Jul-1999
C:Accession: G30603
R:Johnson, N.A.; Carland, F.; Allen, P.M.; Glincher, L.H.
J. Immunol. 142, 3298-3304, 1989
A:Title: T cell receptor gene segment usage in a panel of hen-egg white lysozyme specific
A:Reference number: A30603; MUID:89215300; PMID:2468715
A:Accession: G30603
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <JCH>
A:Cross-references: GB:M26423; NID:G862436; PIDN:AAA68454.1; PID:G862437
A:Note: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match      13.7%; Score 86.5; DB 2; Length 95;
Best Local Similarity 30.3%; Pred. No. 0.12;
Matches 30; Conservative 15; Mismatches 37; Indels 17; Gaps 5;

Qy      19 LPCSFNASQGRLAIGSVTWFRDEVVPGKEVR-----NGTPFRGRGLAPLASSRFLHDH 71
Db      2 LNCTFSDASQY----FAWYRQH--SGKAPKALTSIFSNGEKE--EGRFTIHLNKAASLH-- 52

Qy      72 QAELHIRDVRGHDAIYVCRVEVLG--GVGTGNGTRLIVE 110
Db      53 -FSLHIRDSQPSDALSALYCAVKANYNLVFGSGTKLTVE 90

RESULT 9
A49056
T-cell receptor alpha chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: A49056; S29928
R:Moss, P.A.; Rosenberg, W.M.; Zintzaras, E.; Bell, J.I.
Eur. J. Immunol. 23, 1153-1159, 1993
A:Title: Characterization of the human T cell receptor alpha-chain repertoire and demon
A:Reference number: A49056; MUID:93238874; PMID:8477809
A:Accession: A49056
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-110 <MOS>
A:Note: sequence extracted from NCB1 backbone (NCBIN:130315, NCBIP:130319)
submitted to the EMBL Data Library, October 1992
A:Reference number: S29928
A:Accession: S29928
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-110 <MO2>
A:Cross-references: EMBL:X68696
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match      13.4%; Score 84.5; DB 2; Length 110;
Best Local Similarity 29.2%; Pred. No. 0.23;
Matches 28; Conservative 15; Mismatches 34; Indels 19; Gaps 5;

Qy      3 VSOPPE-IRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAP 61
Db      25 VTQSPEARLQEGESSLNCSTYVS----GARGFWRQD--PKG-----GPEFLFLYS 73

Qy      62 LASSR-----FLHDHQAELHIRDVRGHDAIYVC 90
Db      74 AGEKEKERLKAULTTKESFLHITAPKEDSATVLC 109

RESULT 10
S03503
T-cell receptor alpha chain V region (5H) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C:Accession: S03503
R:Winkto, A.; Mjolsness, S.; Hood, L.
Nature 316, 832-836, 1985
A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.
A:Reference number: S03503; MUID:85296332; PMID:2953908
A:Accession: S03503
A:Molecule type: DNA
A:Residues: 1-112 <WIN>
A:Cross-references: EMBL:X02833; NID:954567; PIDN:CAA26597.1; PID:G54568
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match      13.1%; Score 83; DB 2; Length 112;
Best Local Similarity 30.6%; Pred. No. 0.32;
Matches 30; Conservative 13; Mismatches 37; Indels 18; Gaps 6;

Qy      3 VSOPPE-IRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVR-----NGTPE 54
Db      24 VQSPESLIIVPEGAMTSLNCTFSDASQY----FAWYRQH--SGKAPKALMSIFSNGEKE 77

Qy      55 FRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRV 92
Db      78 -EGRFTIHLNKAASLH---FSLHIRDSQPSDALSALYCAV 111

RESULT 11
PH1671
Ig heavy chain V region (clone 3C9) - human (fragment)

```

C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1671
R;Hillson, J.L.; Katzr, N.S.; Opplinger, I.R.; Sassi, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1671
A;Molecule type: mRNA
A;Residues: 1-109 <HL>
A;Cross-references: UNIPROT:Q9UL89
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;/90/Domain: immunoglobulin homology <IMM>

Query Match 13.1%; Score 82.5; DB 2; Length 109;
Best Local Similarity 24.5%; Pred.No. 0.35;
Matches 26; Conservative 17; Mismatches 48; Indels 15; Gaps 3;

OY 14 GSSAFPLPCFNASQCGLAGTSVTFPRD-----EVVPGEKVENGTPEFRGLAPLA 63
DB 7 GGSVKVSC--KASGGTFSVAISWVRQAQGGLWNGRIPIILGIANYAQKFQGRVTITA 64

OY 64 SSRFLDHQAEHLIRVDVRGHDASIYVCREVVLGLGVGTGNTRLVV 109
DB 65 DK---STSYAYMELSLRSDEDTAVYICAWTNWSSGDYWGQGITLVTV 107

RESULT 12

S57889
T cell receptor Er3 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57889
R;Giegrich, G.; Pette, M.; Mainl, E.; Epplen, J.T.; Wekerle, H.; Hinckanan, A.
Eur. J. Immunol. 22, 753-758, 1992
A;Title: Diversity of T cell receptor alpha and beta chain genes expressed by human T cell hybridomas
A;Reference number: S57869; MUID:92192091; PMID:1372258
A;Accession: S57889
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <IE>
A;Cross-references: EMBL:X57532; NID:g642982; PIDN:CAA40753.1; PID:g642983
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 12.8%; Score 81; DB 2; Length 111;
Best Local Similarity 29.5%; Pred.No. 0.51;
Matches 33; Conservative 16; Mismatches 45; Indels 18; Gaps 5;

OY 6 PPBIRTLEGSSELPFCFNASQGRLAGSVTFWRDEVPGKEV-----RNQTPEFRGR 58
DB 6 PAALSVPEGENVLCVSFTDS----AIYNLOWFRQD--PKGILTSLLLTCSSQREOTSGR 59

OY 59 L-APLASSRPLPHQHQLHRLDRVRGHDAISIYVCREVVLGLGVGTGNTRLVV 109
DB 60 LNNSLDKS----SCRSTLYIAASQGDSDATYLCVCSGTASKLTFTGTGLQV 107

RESULT 13

S40133
T-cell receptor V-alpha w30 - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S40133
R;Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A;Reference number: S40133
A;Accession: S40133
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <PLA>

	Query Match	12.8%;	Score 79.5;	DB 2;	Length 120;
	Best Local Similarity	23.3%;	Pred. No. 0.78;		
	Matches	27;	Conservative	22; Mismatches	49; Indels
	Gaps	15;			
Qy	5 QPEIITLGGSNFLPCCSNAGSRIALGISTVWFRDEVVP	-----KXVRNGTPEPRGR	58		
	: : : : : : : : :				
Db	12 RPPLHSVRGDSAVIICTTDPSNYFF---WKQE--PGAGLQLMLKFSTEINEQG	65			
	: : : : : : : : :				
Qy	59 LAPLASSRFLPHDQAELHIRDVRGHDAISIVCRVEV-LGLGVGTGNGTRLVVE	110			
	: : : : : : : : :				
Db	66 GTVLINK-KKKQLSLNTAAHGSGSYFCAVRANMGYKLFTFGTGTSLLVD	116			
	: : : : : : : : :				

Search completed: November 16, 2004, 23:44:29
Job time : 38 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 16, 2004, 23:31:10 ; Search time 190 Seconds
(without alignments)
363.395 Million cell updates/sec

Title: US-10-036-444-4
Perfect score: 632
Sequence: 1 LWSVQPEIRLTGSSAFPLP.....TNGTFLVVEKHPQLGAGT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 393250

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	14.1	108	Q8JJ25	O8JJ25 orectolobus
2	85.5	13.5	115	Q9BZK2	Q9BZK2 homo sapien
3	80	12.7	120	BAD00300	BAD00300 camelus d
4	79.5	12.6	112	Q96JD2	Q96JD2 homo sapien
5	78.5	12.4	103	Q8JFH2	Q8JFH2 ginglymosto
6	78.5	12.4	111	LV2G HUMAN	P01710 homo sapien
7	78	12.3	113	Q8AXT4	Q8AXT4 ginglymosto
8	76.5	12.1	111	Q6XIE7	Q6XIE7 orectolobus
9	76.5	12.1	111	AAP86761	AAP86761 orectolob
10	75	11.9	116	BAD00224	BAD00224 camelus d
11	74.5	11.8	111	LV1D HUMAN	P01702 homo sapien
12	74.5	11.8	116	Q96JD0	Q96JD0 homo sapien
13	74	11.7	112	BAD00371	BAD00371 camelus d
14	74	11.7	119	BAD00472	BAD00472 camelus d
15	73.5	11.6	106	LV4E HUMAN	P01716 homo sapien
16	73.5	11.6	108	LV5A HUMAN	P01719 homo sapien
17	73.5	11.6	111	LV2D HUMAN	P01707 homo sapien
18	73.5	11.6	111	LV2H HUMAN	P01711 homo sapien
19	73.5	11.6	114	Q8HYT0	Q8HYT0 mogera wogu
20	73	11.6	110	KV15 RABIT	Q8HYT0 orectolagus
21	72.5	11.5	96	Q6P399	Q6P399 mus musculu
22	72.5	11.5	96	AAH64122	AAH64122 mus muscu
23	72.5	11.5	111	LV3B HUMAN	P80748 homo sapien
24	71.5	11.3	84	O19086	O19086 sus scrofa
25	71.5	11.3	113	Q8AXH6	Q8AXH6 ginglymosto
26	71.5	11.3	118	LV39 MOUSE	P01809 mus musculu
27	71	11.2	113	Q8AXT5	Q8AXT5 ginglymosto
28	71	11.2	120	BAD00203	BAD00203 camelus d
29	70.5	11.2	107	LV4C HUMAN	P01717 homo sapien
30	70.5	11.2	115	1 KV02 RABIT	P01683 orectolagus
31	70.5	11.2	116	Q9UL89	Q9UL89 homo sapien

32	70	11.1	117	2	BAD00396	BAD00396 camelus d
33	70	11.1	119	2	BAD00552	BAD00552 camelus d
34	69	10.9	119	1	HV37 MOUSE	P01807 mus musculu
35	68.5	10.8	109	2	Q8JFNO	Q8JFNO ginglymosto
36	68.5	10.8	116	2	BAD00466	BAD00466 camelus d
37	68	10.8	104	2	Q8AXG1	Q8AXG1 ginglymosto
38	68	10.8	112	1	LV1B HUMAN	P01700 homo sapien
39	68	10.8	112	1	LV6A HUMAN	P01721 homo sapien
40	68	10.8	119	1	HV40 MOUSE	P01810 mus musculu
41	68	10.8	120	2	BAD00257	BAD00257 camelus d
42	67.5	10.7	110	2	Q8TE63	Q8TE63 homo sapien
43	67	10.6	105	2	Q8HYT6	Q8HYT6 orectolagus
44	67	10.6	108	2	Q8JJ24	Q8JJ24 orectolobus
45	66.5	10.5	114	2	Q8HYU0	Q8HYU0 bos taurus

ALIGNMENTS

RESULT 1		PRELIMINARY;		PRT; 108 AA.	
Q8JJ25	Q8JJ25	Q8JJ25	Q8JJ25	Q8JJ25	Q8JJ25
AC	Q8JJ25	AC	Q8JJ25	AC	Q8JJ25
DT	01-OCT-2002 (Tremblrel. 22, Created)	DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)	DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)	DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)	DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE	New antigen receptor variable domain (Fragment).	DE	New antigen receptor variable domain (Fragment).	DE	New antigen receptor variable domain (Fragment).
OS	Orectolobus maculatus (spotted wobbegong).	OS	Orectolobus maculatus (spotted wobbegong).	OS	Orectolobus maculatus (spotted wobbegong).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC	Elasmobranchii; Galeomorphii; Galeoidea; Vertebrata; Chondrichthyes;	OC	Elasmobranchii; Galeomorphii; Galeoidea; Vertebrata; Chondrichthyes;	OC	Elasmobranchii; Galeomorphii; Galeoidea; Vertebrata; Chondrichthyes;
OC	Orectolobidae; Orectolobus.	OC	Orectolobidae; Orectolobus.	OC	Orectolobidae; Orectolobus.
NCBI	NCBI TaxID=168098;	NCBI	NCBI TaxID=168098;	NCBI	NCBI TaxID=168098;
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=21956454; PubMed=11959108;	RX	MEDLINE=21956454; PubMed=11959108;	RX	MEDLINE=21956454; PubMed=11959108;
RA	Nuttall S.D., Krishnan U.V., Doughty L., Nathanielsz A., Ally N.,	RA	Nuttall S.D., Krishnan U.V., Doughty L., Nathanielsz A., Ally N.,	RA	Nuttall S.D., Krishnan U.V., Doughty L., Nathanielsz A., Ally N.,
RA	Pike R.N., Hudson P.J., Kortt A.A., Irving R.A.;	RA	Pike R.N., Hudson P.J., Kortt A.A., Irving R.A.;	RA	Pike R.N., Hudson P.J., Kortt A.A., Irving R.A.;
RT	"A naturally occurring NAR variable domain binds the Kgp protease from	RT	"A naturally occurring NAR variable domain binds the Kgp protease from	RT	"A naturally occurring NAR variable domain binds the Kgp protease from
RT	Porphyromonas gingivalis."	RT	Porphyromonas gingivalis."	RT	Porphyromonas gingivalis."
RL	FEBS Lett. 516:80-86(2002).	RL	FEBS Lett. 516:80-86(2002).	RL	FEBS Lett. 516:80-86(2002).
DR	EMBL; AF466395; AAM33845.1; -	DR	EMBL; AF466395; AAM33845.1; -	DR	EMBL; AF466395; AAM33845.1; -
DR	HSPF; P01825; 1BEQ.	DR	HSPF; P01825; 1BEQ.	DR	HSPF; P01825; 1BEQ.
DR	GO; GO:0004872; F:receptor activity; IEA.	DR	GO; GO:0004872; F:receptor activity; IEA.	DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR003599; IG.	DR	InterPro; IPR003599; IG.	DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.	DR	InterPro; IPR007110; IG-like.	DR	InterPro; IPR007110; IG-like.
DR	Pfam; PF00047; Ig; 1.	DR	Pfam; PF00047; Ig; 1.	DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00409; IG; 1.	DR	SMART; SM00409; IG; 1.	DR	SMART; SM00409; IG; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.	DR	PROSITE; PS50835; IG_LIKE; 1.	DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Receptor.	KW	Receptor.	KW	Receptor.
FT	NON_TER 1	FT	NON_TER 1	FT	NON_TER 1
FT	NON_TER 108	FT	NON_TER 108	FT	NON_TER 108
SEQUENCE	108 AA; 11778 MW; 90A480F1A6409BB7 CRC64;	SEQUENCE	108 AA; 11778 MW; 90A480F1A6409BB7 CRC64;	SEQUENCE	108 AA; 11778 MW; 90A480F1A6409BB7 CRC64;
Query Match		14.1%; Score 89; DB 2; Length 108;			
Best Local Similarity		29.8%; Pred No. 0.34;			
Matches		34; Conservative 13; Mismatches 53; Indels 14; Gaps 5;			
QY	3	VSQPEIRLTLE-GSSAFPLCPFNASQGRLAIGSVYTFRDEVYVPGKEVRNGTFEGRGLAP 61			
Db	3	VQDPRIATKGTGSLTINCVLRTD--ACALDSTNWTYTKLGSTKE---QTISIGGRYSE 57			
QY	62	LASRFLDHQAEHLHIRDVRGHDSAIYCVRYE-----VLGLGVGTGNGTRLVVE 110			
Db	58	TVDE---GSNSASLTIRDLRVDSGTGYCKAYRCAFNFTGVGYKEGAGTILTVK 108			
RESULT 2		PRELIMINARY;		PRT; 115 AA.	
Q9BZK2	Q9BZK2	Q9BZK2	Q9BZK2	Q9BZK2	Q9BZK2
AC	Q9BZK2	AC	Q9BZK2	AC	Q9BZK2
DT	01-JUN-2001 (Tremblrel. 17, Created)	DT	01-JUN-2001 (Tremblrel. 17, Created)	DT	01-JUN-2001 (Tremblrel. 17, Created)
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)	DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)	DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)	DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)	DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)

```

DE CTLA-4 V domain region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu N., Yu S.;
RT "The DNA sequence and PCR-SSCP analysis of three CTLA-4 gene V domain
RT in Chinese.";
RL Chin. J. Microbiol. Immunol. 14:349-352(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhu N., Yu S.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF316875; AAK13084.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig; 1.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00406; IGV; 1.
FT NON TER 115
FT NON TER 115
SQ SEQUENCE 115 AA; 12347 MW; 473A2C73D5BA368E CRC64;

Query Match 13.5%; Score 85.5; DB 2; Length 115;
Best Local Similarity 27.7%; Pred. No. 0.83;
Matches 33; Conservative 15; Mismatches 52; Indels 19; Gaps 4;

QY 3 VSQPPETRTLEGSAPLPCSFNASQGLRAIGSVTWFRDEVVPGKEVNRNTPFRGLAPL 62
DB 3 VAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNELT-- 59
QY 63 ASSREFLD-----HQAELHIRDVRGHDAIYVCRVEVL---GLGVGTGNGRLVV 109
DB 60 ----FLDDSICTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYILGNGTIYV 114

RESULT 3
BAD00300 PRELIMINARY; PRT; 120 AA.
AC BAD00300;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGTV.
OS Camelus dromedarius (Dromedary) (Arabic camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
CX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091938; BAD00300.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 120 AA; 13084 MW; 91760CE242608D9E CRC64;

Query Match 12.7%; Score 80; DB 2; Length 120;
Best Local Similarity 29.7%; Pred. No. 3.2;
Matches 33; Conservative 10; Mismatches 46; Indels 22; Gaps 6;

QY 14 GSSAFPLPCSFNASQGLRAIGSVTWFRDEVVPGKEVRN-----GTPEFRGLAPLAS 64
DB 15 GGSLLTSLCTAPEYTGILT-CMGWFRQ--VPGKEREEVAYIGARSYYTDSVGR---FTI 67

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QY 65 SRFLDHQAELHIRDVRGHDAIYVC---RVEVLGLG---VGTGNGTRLVV 109
DB 68 SRDNYKNVQLHMTRLTPTDGYCCAKETGYCGLGGNTDNGRGTFQTV 118

RESULT 4
Q96JD2 PRELIMINARY; PRT; 112 AA.
AC Q96JD2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid lambda 6 light chain variable region NEG (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267873; AAK58585.1; -.
DR HSSP; P06317; 1CD0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

Query Match 12.6%; Score 79.5; DB 2; Length 112;
Best Local Similarity 26.7%; Pred. No. 3.3;
Matches 32; Conservative 19; Mismatches 44; Indels 25; Gaps 7;

QY 3 VSQPPETRTLEGSAPLPCSFNASQGLRAIGSVTWFRDEVVPG-----KEVRNGT 52
DB 4 LTQPHSVSGSPGKTTITISCT--GSSGRASNSQVQYQQR--PGSAPNIWYNNQPSGV 59
QY 53 PE-FRGLAPLASSRFLHQAELHIRDVRGHDAIYVCRV--EVLGLGVGTGNGTRLVV 109
DB 60 PDRFSGSIDSSNS-----ASLTISGLMTDEADYVQCQSFDDSTNQGV-FGGGTRLTV 111

RESULT 5
Q8JFH2 PRELIMINARY; PRT; 103 AA.
AC Q8JFH2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Antigen receptor (Fragment).
GN Name=NAR;
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC Ginglymostomatidae; Ginglymostoma.
CX NCBI_TaxID=7801;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epigonal;
RA Diaz M., Stanfield R.L., Greenberg A.S., Flajnik M.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114932; AAK76235.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.

```

FT NON TER 1 1
FT NON TER 103 103
SQ SEQUENCE 103 AA; 10816 MW; EB5D3A9755AC8504 CRC64;

Query Match 12.4%; Score 78.5; DB 2; Length 103;
Best Local Similarity 25.0%; Pred. No. 3.8;
Matches 30; Conservative 11; Mismatches 46; Indels 33; Gaps 5;

QY 3 VSOPPEIRTELE-GSSAFPLPCSFNASQGLAIGSVTWFR-----DEVVPG-----KEVR 49
Db 2 VDTQPSRVTKETGESLTINCVL-R--DASYALGTCWYRKSGSTNEESISKGRYVETVN 59
QY 50 NGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTGNGTRLV 109
Db 60 SGSKSF-----SLRINDLTVEDGTYRCGAAGVGLDAACGDGTAFTV 101

RESULT 6
LV2G_HUMAN STANDARD; PRT; 111 AA.
AC P01710;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-II region BO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=71103825; PubMed=5532228;
RA Winkler M., Futnani F.W.;
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
RT chymotryptic peptides, and sequence of protein Bo.";
RL J. Biol. Chem. 245:4488-4507(1970).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PR; A01376; LHUBO.
DR HSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 106
FT MOD RES 1 1
FT DISULFID 22 90
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 12.4%; Score 78.5; DB 1; Length 111;
Best Local Similarity 24.0%; Pred. No. 4.1;
Matches 29; Conservative 19; Mismatches 44; Indels 29; Gaps 6;

QY 3 VSOPPEIRTELE-GSSAFPLPCSFNASQGLAIGSVTWFRDEVVPGKEVR-----49
Db 4 LTQPPSASGSPGQSVTIISCTGTSSD-----VGDNKYVSWYQQH--PGRAPKLVIIEVSQRP 57
QY 50 NGTPE-FRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTGNGTRLV 108
Db 58 SGVPDRFSGSKS-----DNTASLTVSLGLRAEDEADYICSSYVDNNNFVGGGKLT 108
QY 109 V 109
Db 109 V 109

RESULT 7
Q8AXI4 PRELIMINARY; PRT; 113 AA.
AC Q8AXI4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Novel antigen receptor (Fragment).
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC Ginglymostomatidae; Ginglymostoma.
CX NCBI_TaxID=7801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22791976; PubMed=12909128;
RA Dooley H., Flajnik M.F., Porter A.J.;
RT "Selection and characterization of naturally occurring single-domain
RT (IgNAR) antibody fragments from immunized sharks by phage display.";
RL Mol. Immunol. 40:25-33(2003).
DR EMBL; AF447096; AAN75852.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMC0409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12042 MW; 71522771FEA75661 CRC64;

Query Match 12.3%; Score 78; DB 2; Length 113;
Best Local Similarity 24.4%; Pred. No. 4.7;
Matches 32; Conservative 10; Mismatches 51; Indels 38; Gaps 5;

QY 3 VSOPPEIRTELE-GSSAFPLPCSFNASQGLAIGSVTWFRDEVVPGKE-----VR 49
Db 3 VDTQPSRVTKETGESLTINCVL-R--DASYALGTCWYRKSGSTNEESISKGRYVETVN 60
QY 50 NGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTGNGTRLV 109
Db 61 SGSKSF-----SLRINDLTVEDGTYRC-----GLGVAGYCDYALC 97
QY 110 EKEHPQLGAGT 120
Db 98 SSRYAECGDGT 108

RESULT 8
Q8XIE7 PRELIMINARY; PRT; 111 AA.
AC Q8XIE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE New antigen receptor variable domain (Fragment).
OS Orectolobus maculatus (spotted wobbegong).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC Orectolobidae; Orectolobus.
CX NCBI_TaxID=168098;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14997552;
RA Nuttall S.D., Humberstone K.S., Krishnan U.V., Carmichael J.A.,
RA Doughty L., Hattarki M., Coley A.M., Casey J.L., Anders R.F.,
RA Foley M., Irving R.A., Hudson P.J.;
RT "Selection and affinity maturation of IgNAR variable domains targeting
RT Plasmodium falciparum AMA1.";
RL Proteins 55:187-197(2004).
DR EMBL; AY281681; AAP86761.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.

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DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12252 MW; EB2C4A74965FC75F CRC64;

Query Match 12.1%; Score 76.5; DB 2; Length 111;
Best Local Similarity 26.0%; Pred. No. 6.6;
Matches 34; Conservative 11; Mismatches 43; Indels 43; Gaps 6;

QY 2 WVSOPPEIRLE-GSSAFPLCSF-NASQRLAIGSVTWFRDEVVPKE----- 47
DB 2 WVDQTPATKGTGESITINCLVDASYG---LESTGWYRTKLGSNTNEQTIISIGRYVET 58
QY 48 VRNGTPEFRGLAPLASSRFLHQAEHLHIDVRGHDASIVYCRVVEVLGLVGVTGN---- 103
DB 59 VNRKGSKF-----SLRIRDURVEDSGTYKCGAFRFLPYGYGSLPLS 100
QY 104 ----GTRLVVE 110
DB 101 EKGAGTVLTVK 111

RESULT 9
AAP86761 PRELIMINARY; PRT; 111 AA.
ID AAP86761;
AC AAP86761;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE New antigen receptor variable domain (Fragment).
OS Orectolobus maculatus (spotted webbing).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Orectolobiformes;
OC Orectolobidae; Orectolobus.
OX NCBI_TaxID=168098;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14997552;
RA Nuttall S.D., Humberstone K.S., Krishnan U.V., Carmichael J.A.,
RA Doughty L., Hattarki M., Coley A.M., Casey J.L., Anders R.F.,
RA Foley M., Irving R.A., Hudson P.J.;
RT "Selection and affinity maturation of IgNAR variable domains targeting
RT Plasmodium falciparum AMA1."
RL Proteins 55:187-197(2004).
DR EMBL; AY261681; AAP86761.1; .
KW Receptor.
FT NON TER 1 1
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12252 MW; EB2C4A74965FC75F CRC64;

Query Match 12.1%; Score 76.5; DB 2; Length 111;
Best Local Similarity 26.0%; Pred. No. 6.6;
Matches 34; Conservative 11; Mismatches 43; Indels 43; Gaps 6;

QY 2 WVSOPPEIRLE-GSSAFPLCSF-NASQRLAIGSVTWFRDEVVPKE----- 47
DB 2 WVDQTPATKGTGESITINCLVDASYG---LESTGWYRTKLGSNTNEQTIISIGRYVET 58
QY 48 VRNGTPEFRGLAPLASSRFLHQAEHLHIDVRGHDASIVYCRVVEVLGLVGVTGN---- 103
DB 59 VNRKGSKF-----SLRIRDURVEDSGTYKCGAFRFLPYGYGSLPLS 100
QY 104 ----GTRLVVE 110
DB 101 EKGAGTVLTVK 111

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RESULT 10
BAD00224 PRELIMINARY; PRT; 116 AA.
ID BAD00224;
AC BAD00224;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IG VH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091862; BAD00224.1; .
FT NON TER 1 1
FT NON TER 116 116
SQ SEQUENCE 116 AA; 12763 MW; C8694D6153CEC34E CRC64;

Query Match 11.9%; Score 75; DB 2; Length 116;
Best Local Similarity 26.9%; Pred. No. 9.9;
Matches 29; Conservative 18; Mismatches 41; Indels 20; Gaps 6;

QY 14 GSSAFPLCSFNASQRLAIGSVTWFRDEVVPKEVR-----NGTPEF-----RGLAP 61
DB 15 GESRLSCA--ASGTFPSWAYMSWFRQ--APGSELEWVSGINSNGSNYYKSLKGS--- 67
QY 62 LASSRFLHQAEHLHIDVRGHDASIVYCRVVEVLGLVGVTGNGTRLV 109
DB 68 FTISRDNKNTLYLQMSLSKSDTALYICNIGQL-LGRSRGGTQTV 114

RESULT 11
LVID_HUMAN
ID LVID_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup."
RL J. Biochem. 93:421-429(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01965; LIHUNG.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
FW Pyrolysine carboxylic acid. Ig-like.
FT DOMAIN 1 105

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=69088380; PubMed=4883841;
RX Milstein C., Clegg J.B., Jarvis J.M.;
RT "immunoglobulin lambda-chains. The complete amino acid sequence of a
RL Bence-Jones protein.";
RL Blochem. J. 110:631-652(1968).
CC -|- MISCELLANEOUS: This is a Bence-Jones protein.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01982; L4HUX.
DR HSP; P06317; LCD0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 102
FT NON TER 106 106 Ig-like.
SQ SEQUENCE 106 AA; 11334 MW; 24D04344AA812855 CRC64;

Query Match 11.6%; Score 73.5; DB 1; Length 106;
Best Local Similarity 25.4%; Pred. No. 13;
Matches 30; Conservative 19; Mismatches 43; Indels 27; Gaps 6;

Qy 3 VSQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFERDEVVPGK-----EVRNGT 52
Db :||| : :||| : :||| : :||| : :||| : :||| : :||| : :||| :
3 LTQPPSVSVSPGQTASITCSGD---KLGDKDVCWYQQR--PGQSPVLVIYQDNQRSSGI 56

Qy 53 PE-FRGLAPLASSRFLHDHQALHIDVRGHDSIYVCRVEVLGLGVGTGNGTRLVV 109
Db |||| : :||| : :||| : :||| : :||| : :||| : :||| :
57 PERFSGSNS-----GNTATLTISGTQAMDEADYQCQAWD-SMSVYVFGGTRLTV 104
```

Search completed: November 16, 2004, 23:42:59
Job time : 191 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 23:30:25 ; Search time 151 Seconds
(without alignments)
285.083 Million cell updates/sec

Title: US-10-036-444-4

Perfect score: 632

Sequence: 1 LWSQPEPTLEGSALFLP.....TGNTRLVVEKHPQLGAGT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1197155

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Genesepc_23Sep04:*

- 1: Genesepc1980s:*
- 2: Genesepc1990s:*
- 3: Genesepc2000s:*
- 4: Genesepc2001s:*
- 5: Genesepc2002s:*
- 6: Genesepc2003as:*
- 7: Genesepc2003bs:*
- 8: Genesepc2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	632	100.0	120	4	Aae02771 Human Nkp
2	632	100.0	120	8	Adq30924 Human Nkp
3	89.5	14.2	110	6	AbR55818 Lambda ch
4	87.5	13.8	115	8	AbO59070 Human gen
5	87.5	13.8	120	3	Aay33700 Cytotoxic
6	85.5	13.5	109	5	Aau83808 MS-GPC-10
7	85.5	13.5	109	5	AbB57568 HLA-DR-sp
8	84.5	13.5	120	2	Aaw41404 Human ant
9	84.5	13.4	110	6	Ada89200 Human ant
10	83.5	13.2	120	2	Aaw41407 Humanised
11	83.5	13.2	120	2	Aaw41403 Humanised
12	81.5	12.9	111	2	Aaw90279 Human ant
13	81.5	12.9	111	3	Aay68807 A light c
14	81.5	12.9	120	2	Aaw41406 Humanised
15	80.5	12.7	110	6	AbR54951 IgG light
16	80.5	12.7	115	2	Aay39548 Human CTL
17	80.5	12.7	118	2	AAR61096 Human can
18	79.5	12.6	108	2	AAR88719 Human ant
19	79.5	12.6	109	5	AbB57570 Human ant
20	79.5	12.6	111	2	AAR12284 Anti-huma
21	78.5	12.4	110	4	Aau02612 Anti-adip
22	78.5	12.4	110	6	AbR54940 IgG light
23	78.5	12.4	110	6	AbR55828 Lambda ch
24	78.5	12.4	111	4	Aau02585 Anti-adip
25	78.5	12.4	120	5	Abp62168 Human imm

26 78 12.3 113 6 ABR43772 G. cirrat
27 77.5 12.3 111 7 ADC03136 Colon spe
28 77.5 12.3 111 7 ADC03142 Colon spe
29 77.5 12.3 112 7 ADC03144 Colon spe
30 76.5 12.1 109 5 AAU83816 MS-GPC-8-
31 76.5 12.1 109 5 ABR57584 HLA-DR-sp
32 76.5 12.1 110 6 ABR54937 Igg light
33 76.5 12.1 111 6 ABU08154 Human Erb
34 76.5 12.1 120 2 AAU41402 Humanised
35 76 12.0 15 4 AAE02774 Human Nkp
36 76 12.0 15 8 ADQ30927 Human Nkp
37 76 12.0 113 4 AAB67068 Human T c
38 76 12.0 114 6 ABP56512 Human ant
39 76 12.0 114 6 ABP56511 Human ant
40 76 12.0 118 4 AAG80213 Human aut
41 76 12.0 118 4 AAU02625 Anti-adip
42 76 12.0 120 4 AAU02608 Anti-adip
43 75.5 11.9 108 2 AAR30146 MAB 1-3-1
44 75.5 11.9 109 4 AAG93668 Human ant
45 75.5 11.9 109 5 AAU83814 MS-GPC-8-

ALIGNMENTS

RESULT 1

AAE02771
ID AAE02771 standard; protein; 120 AA.

XX AC AAE02771;

XX DT 06-AUG-2001 (first entry)

XX DE Human Nkp30 receptor extracellular region sequence.

XX KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
XX KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
XX KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
XX KW therapy; extracellular region.

XX OS Homo sapiens.

XX PN WO200136630-A2.

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-EP011697.

XX PR 15-NOV-1999; 99CA-02288307.

XX PR 15-NOV-1999; 99US-00440514.

XX PA (INNA-) INNATE PHARMA SAS.

XX PY (UYGE-) UNIV GENOVA.

XX R Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

XX Novel compound, useful for detection and/or quantifying the presence of
XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX Claim 1; Fig 7B; 83pp; English.

XX The invention relates to human Nkp30 receptor and its corresponding cDNA
XX molecule which is involved in natural cytotoxicity mediated by natural
XX killer (NK) cells and antibodies that identify the same. Nkp30 receptor
XX is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
XX expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
XX useful for detecting and/or quantifying the presence of NK cells in a
XX biological sample. The invention also provide kits for detecting and/or
XX quantifying the presence of NK cells, for the selective removal of NK
XX cells from a biological sample, for the positive and selective
XX purification of NK cells from a biological sample and for the in vitro

CC stimulation of NK cell cytotoxicity. The invention further provides a
 CC pharmaceutical composition which is used as a drug for grafting
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft
 CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for
 CC the prevention, palliation and/or therapy of solid or liquid tumours,
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
 CC microorganism, notably viral infection. NKp30 antibodies are useful for
 CC identifying NKp30 natural ligands and allow assessment of the level of
 CC surface NKp30 ligand expressed on an NK-susceptible target cell and the
 CC comparison of this level to the standard physiological one. Hence NKp30
 CC antibodies are useful in the diagnosis of tumours or of infection. The
 CC present sequence is the extracellular region of human NKp30 receptor
 XX
 XX Sequence 120 AA;

Query Match 100.0%; Score 632; DB 4; Length 120;
 Best Local Similarity 100.0%; Pred No. 2e-62;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA 60
 DB 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA 60

QY 61 PLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGVLGVTGNGTGLVVEKEHPQLGAGT 120
 DB 61 PLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGVLGVTGNGTGLVVEKEHPQLGAGT 120

RESULT 2
 ADQ30924
 ID ADQ30924 standard; protein; 120 AA.
 XX
 AC ADQ30924;
 XX
 XX 23-SEP-2004 (first entry)
 DT Human NKp30 extracellular region.
 DE
 DE Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.
 KW
 XX Homo sapiens.
 OS
 XX WO2004056392-A1.
 PN
 XX 08-JUL-2004.
 PD
 XX 22-DEC-2003; 2003WO-EP014716.
 PF
 XX 23-DEC-2002; 2002US-0435344P.
 PR
 XX (INNA-) INNATE PHARMA.
 PA
 XX Romagne F, Andre P;
 PI
 XX WPI; 2004-507595/48.
 DR
 XX Pharmaceutical compositions that stimulate proliferation of natural
 XX killer cells useful for therapy of melanoma, chronic myeloid, and
 XX leukemia, comprise an anti-natural killer cell receptor antibody and
 XX interleukins.
 PT
 XX Claim 3; SEQ ID NO 2; 35pp; English.

XX The present sequence is that of the extracellular region of human NKp30
 XX ADQ30923, a 190 amino acid polypeptide that is selectively expressed by
 XX natural killer (NK) cells, and particularly by mature NK cells. Claimed
 XX pharmaceutical compositions that have a stimulating effect on the
 XX proliferation of NK cells comprise an antibody such as an anti-NKp30
 XX antibody or anti-NKp46 antibody or its immuno-reactive fragment and a
 XX cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
 XX antibody(ies) and cytokine(s) being administered together or separately
 XX to a subject. The anti-NKp30 antibody is an isolated antibody or its
 XX antigen-binding fragment which specifically binds to NKp30 or to a

CC fragment, including the extracellular region, of NKp30. The
 CC pharmaceutical compositions, when used for daily subcutaneous injection,
 CC comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and
 CC lower than 1 million units/square meters/day of cytokine(s), are useful
 CC for the prevention, palliation and therapy of e.g. melanoma, chronic
 CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
 XX prevention, palliation and therapy (claimed).

XX Sequence 120 AA;

Query Match 100.0%; Score 632; DB 8; Length 120;
 Best Local Similarity 100.0%; Pred No. 2e-62;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA 60
 DB 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA 60

QY 61 PLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGVLGVTGNGTGLVVEKEHPQLGAGT 120
 DB 61 PLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGVLGVTGNGTGLVVEKEHPQLGAGT 120

RESULT 3
 ABR55818
 ID ABR55818 standard; protein; 110 AA.
 XX
 AC ABR55818;
 XX
 XX 02-SEP-2003 (first entry)
 DT
 XX Lambda chain variable region of anti-Ang-2 antibody G1D4 lambda.
 DE
 DE Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
 KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
 KW angiogenesis; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 22..36
 FT /note= "complementarity determining region (CDR) 1"
 FT Region 58..80
 FT /note= "complementarity determining region (CDR) 2"
 FT Region 91..101
 FT /note= "complementarity determining region (CDR) 3"
 FT
 XX WO2003030833-A2.
 PN
 XX 17-APR-2003.
 PD
 XX 11-OCT-2002; 2002WO-US032613.
 PF
 XX 11-OCT-2001; 2001US-0328604P.
 PR
 XX 10-OCT-2002; 2002US-00269805.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Olinier JD;
 PI
 XX WPI; 2003-504963/47.
 DR
 XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
 XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
 XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 XX Claim 1; Page 95; 161pp; English.

XX The invention relates to a specific binding agent, which comprises at
 XX least one peptide selected from any of 62 peptides (ABR55789-830) or its
 XX fragment. The binding agents are antibodies that recognize and bind to
 XX angiotensin-2 (Ang-2). The specific binding agent, particularly the

CC antibody, is useful for inhibiting undesired angiogenesis, treating
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC 2 activity, modulating vascular permeability or plasma leakage, or
CC treating a disease (e.g. ocular neovascular disease, obesity,
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a lambda chain variable region of an anti-Ang-2
CC antibody
XX
XX Sequence 110 AA;
Query Match 14.2%; Score 89.5; DB 6; Length 110;
Best Local Similarity 26.3%; Pred. NO. 0.075;
Matches 31; Conservative 20; Mismatches 44; Indels 23; Gaps 6;
QY 3 VSPQPIRTLESSALPCSFNASQGLAIGSVTFRDEWPG-----KEVRNGT 52
DB 4 LQPHSVSSSPKTVIPCT--RSSGSIASNVQWFKR--FGSAPSVIYEDKRPQGV 59
QY 53 PE-FRGLAPLASSRFLHDHQAELHIRDVGRHDASIYVCRVGLGVGTGNGTRLVV 109
DB 60 PDFSSGIDSSNS-----ASLTISGLKTEADYCYQ-SYNSRGVMFGGTXLTV 109
RESULT 4
ID ABO59070 standard; protein; 115 AA.
AC ABO59070;
XX
XX 29-JUL-2004 (first entry)
DT
DE Human genome derived single exon protein #5304.
KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
OS
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX Claim 45; SEQ ID NO 32704; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above). The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX Sequence 115 AA;
Query Match 13.8%; Score 87.5; DB 8; Length 115;
Best Local Similarity 34.0%; Pred. No. 0.13;
Matches 32; Conservative 9; Mismatches 34; Indels 19; Gaps 6;
QY 9 IRTLEGSSALPCSFNASQGLAIG-SVTFRDEWPGKEV---RNG-----TPEPR 56
DB 11 IRALVGDEVELFC--RSPGKNATGMEVGYRP---PFSRVVHLRYNGKDDGQDAPEYR 65
QY 57 GRLAPLASSRFLHDHQAELHIRDVGRHDASIYVC 90
DB 66 GRTELLKDA--IGSGKVTLRIRNVRFSDGGFTC 97
RESULT 5
AAAY93700
ID AAY93700 standard; protein; 120 AA.
XX
XX AC AAY93700;
XX
XX 03-OCT-2000 (first entry)
DT
DE Cytotoxic T-lymphocyte antigen (CTLA)-4 peptide.
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX proliferative disorder; cancer; immunodeficient disorder.
XX
XX Homo sapiens.
OS
XX WO2000037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 98WO-US030895.
XX
XX 23-DEC-1998; 98US-0113647P.
XX (PFIZ) PRIZER INC.
XX (ABGE-) ARGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvalan JR;
XX WPI; 2000-442647/38.
XX
XX

PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
 PT -4 containing specified heavy and light chain sequences, useful for
 XX treating, e.g. immune disorders.
 XX
 PS Example 1; Page 60; 157pp; English.
 XX
 CC The present sequence represents a cytotoxic T-lymphocyte antigen (CTLA)-4
 CC peptide. The specification describes an antibody which is capable of
 CC binding CTLA-4. The antibody is composed of a heavy chain variable
 CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
 CC encoded by a human VH3-33 family gene. The modifications are contained in
 CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
 CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
 CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
 CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
 CC used to up-regulate immune system to up-regulate immunodeficient
 CC disorders
 CC
 SQ Sequence 120 AA;
 Query Match 13.8%; Score 87.5; DB 3; Length 120;
 Best Local Similarity 27.4%; Pred. No. 0.14;
 Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;
 QY 3 VSQPPERTLEGSAFLPCSFNASQGLAIGSWTFRDEWVPGKEVRNGTPEFRGLAPL 62
 DB 3 VAGPAVVLASSRGIASEVCEY-ASPKATEVRVTVLROADSQTEVCAATYMGNELT-- 59
 QY 63 ASSRFUHD-----HQAELHIRDVRGHDAIYVCRVEVL---GLGVGTGNGRLVVE 110
 DB 60 ----FLDDSICTGTSGNQVNLTIQGLRAMDTGLYCKVELMYPYPYILGNGTQIYVI 115
 QY 111 KEHP 114
 DB 116 DPEP 119
 RESULT 6
 AAU83808
 ID AAU83808 standard; protein; 109 AA.
 XX AAU83808;
 AC AAU83808;
 DT 08-MAY-2002 (first entry)
 XX MS-GPC-10 light chain variable region.
 DE
 XX Human; antibody-based antigen; HLA-DR; VL; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; light chain variable region.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO2001187337-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US015625.
 XX
 PR 12-MAY-2000; 2000EP-00110065.
 PR 06-OCT-2000; 2000US-0238492P.
 XX
 XX (GPCB-) GPC BIOTECH AG.
 PA (MORP-) MORPHOSYS AG.
 XX
 XX Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
 XX

DR WPI; 2002-075288/10.
 XX Polypeptide compositions which bind to cell surface epitopes, which in
 PT multivalent form kills lymphoid tumor cells and in monovalent form causes
 PT immunosuppression or inhibits activation of lymphocytes.
 XX
 PS Claim 22; Fig 15; 150pp; English.
 XX
 CC The invention relates to a composition which includes a polypeptide or a
 CC multivalent polypeptide comprising one or more antibody-based antigen -
 CC binding domain of human composition with binding specificity for an
 CC antigen expressed on surface of a human cell, especially HLA-DR (human
 CC leukocyte antigen DR), where treating cells expressing HLA-DR with the
 CC multivalent polypeptide causes or leads to killing of cells without need
 CC of cytotoxic entities or immunological mechanisms. Also included are the
 CC nucleic acid encoding the polypeptide, a vector comprising the nucleic
 CC acid and a host cell harbouring vector or nucleic acid. The polypeptide
 CC (optionally linked to cytotoxic or immunogenic agent), the nucleic acid
 CC and the host cell are useful for preparing a pharmaceutical preparation
 CC for the treatment of cell proliferative disorders, disorders involving
 CC transformed cells expressing MHC class II antigens, B cell non-Hodgkin's
 CC lymphoma, Hodgkin's lymphoma, hairy cell leukaemia, acute myeloid
 CC leukaemia, T cell lymphoma, T cell non-Hodgkin's lymphoma, chronic
 CC myeloid leukaemia, chronic lymphoid leukaemia or multiple myeloid
 CC leukaemia, disorders involving unwanted activation of the cells of the
 CC immune system, such as lymphoid cells expressing MHC class II, rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft vs.
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
 CC antigen is useful for suppressing activation or proliferation of a cell
 CC of the immune system, suppressing interleukin-2 (IL-2) secretion by a
 CC cell of the immune system, such as expressing HLA-DR, the interaction of
 CC the cell of the immune system with another cell, immunosuppressing a
 CC patient and for killing a cell expressing an antigen, HLA-DR on the
 CC surface of the cell, where neither cytotoxic entities nor immunological
 CC mechanisms are needed to cause or lead to the killing. The killing is
 CC dependent on the action of non-caspase proteases and/or cannot be
 CC inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a light chain
 CC variable region containing CDRs (complementarity determining region)
 CC based on the human antigen binding polypeptides of the invention MS-GPC-
 CC 1, 6, 8 and 10. The CDRs are either the native sequence or have been
 CC optimised/mutated to alter their antigen binding capabilities
 XX
 SQ Sequence 109 AA;
 Query Match 13.5%; Score 85.5; DB 5; Length 109;
 Best Local Similarity 26.7%; Pred. No. 0.21;
 Matches 32; Conservative 22; Mismatches 37; Indels 29; Gaps 7;
 QY 3 VSQPPERTLEGSAFLPCSFNASQGLAIGS--VTMFRDEVVPGKEVR-----N 50
 DB 4 LTQPPFVSAGPQGRVITSCGSSN----IGSNVSNYQQ--LFGTAPKLLIYDNNQRP 57
 QY 51 GTPE-FRGLAPLASSRFLHDQAELHIRDVRGHDAIYVCRVEVLGLGVGTGNGRLV 109
 DB 58 GVPDRFSGSKSGTSAS-----LAITGLQSEADYVCQSYDLTMGV-FGGTFLAV 107
 RESULT 7
 ABB57568
 ID ABB57568 standard; peptide; 109 AA.
 XX ABB57568;
 AC ABB57568;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE HLA-DR-specific protein MS-GPC-10 VL sequence.
 PI Immunomodulatory human MHC class II antigen-binding protein; HLA;
 KW


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XX 17-OCT-2003 (revised)
DT 02-JUN-1998 (first entry)
XX
DE Humanised antibody 806.077 HuVH3 chain.
XX
XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
XX cancer diagnosis; complementarity determining region; Fd chain.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
XX WO9742329-A1.
XX
XX 13-NOV-1997.
XX
XX 29-APR-1997; 97WO-GB001165.
XX
XX 04-MAY-1996; 96GB-00009405.
XX
XX 14-FEB-1997; 97GB-00003103.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Copley CG, Edge MD, Emery SC;
XX
XX WPI; 1997-558987/51.
XX
XX N-PSDB; AAV17307.
XX
XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis
XX and therapy of cancer.
XX
XX Example 12; Page 144; 208pp; English.
XX
XX This sequence is the HuVH3 region of the antibody of the invention. The
XX antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab).
XX Host cells or transgenic organisms transformed with DNA encoding the
XX antibody, are used to make the antibody or conjugate. The conjugate is
XX used in a medicament suitable for intravenous administration. The
XX conjugate can be used for cancer therapy, selectively killing tumour
XX cells. The antibody can be used for in vivo or in vitro diagnosis of
XX cancer. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 120 AA;
XX
Query Match 13.2%; Score 83.5; DB 2; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.39;
Matches 31; Conservative 11; Mismatches 34; Indels 39; Gaps 6;
XX
QY 2 WVSQPEIRTLGGSAFLPCSFNASQGRLAGSVTWFRDEVVPGKEVRNG---TPEPRG 57
Db 36 WVRQPP-----GR-GLEWIGWIDPE-----NGDTEYAPKFRG 66
XX
QY 58 RLAPLASSRFLHDHQAELHIRDVGRGHDASIYVCRVEVLGLVGVT---GNGTRLVW 109
Db 67 RVTWLADS---SKNQASRLSSVTAADTAVYCHVLIYAGYLANDVWGQGLTVTV 118
XX
RESULT 12
AAW90279
ID AAW90279 standard; protein; 111 AA.
XX
XX AAW90279;
XX
XX 07-SEP-1999 (first entry)
XX
XX Human anti-GPIIb/IIIa antibody light chain protein from phagemid PDG7.
XX
XX Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
XX blood platelet membrane protein; predisposition; prevention; treatment;
XX autoimmune thrombocytopaenic purpura; AITP; fibrinogen binding; thrombi;
XX thrombocyte; cardiac infarction; pulmonary embolism; light chain.
XX

```

```

OS Homo sapiens.
XX
XX Key
XX Region
XX Location/Qualifiers
XX 1..20
XX /label= FR1
XX /note= "framework region 1"
XX 21..33
XX /label= CDR1
XX /note= "complementarity determining region 1"
XX 34..48
XX /label= FR2
XX /note= "framework region 2"
XX 49..55
XX /label= CDR2
XX /note= "complementarity determining region 2"
XX 56..87
XX /label= FR3
XX /note= "framework region 3"
XX 88..98
XX /label= CDR3
XX /note= "complementarity determining region 3"
XX 99..111
XX /label= FR4
XX /note= "framework region 4"
XX
XX WO9855619-A1.
XX
XX 10-DEC-1998.
XX
XX 05-JUN-1998; 98WO-EP003397.
XX
XX 06-JUN-1997; 97DE-01023904.
XX
XX 12-DEC-1997; 97DE-0105227.
XX
XX 08-MAY-1998; 98DE-01020663.
XX
XX (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
XX
XX Berchtold P, Escher RFA;
XX
XX WPI; 1999-105496/09.
XX
XX N-PSDB; AAV72224.
XX
XX Nucleic acid encoding human autoantibodies against platelet glycoprotein
XX IIb/IIIa used for diagnosis, treatment and prevention of autoimmune
XX thrombocytopaenic purpura and for modulation of fibrinogen binding.
XX
XX Disclosure; Page 50; 93pp; German.
XX
XX This invention describes novel nucleic acid fragments that encode human
XX auto-antibodies and anti-idiotypic antibodies against blood platelet
XX membrane protein, GPIIb/IIIa. The products of the invention are used for
XX diagnosis (including monitoring and determining predisposition), (AITP)
XX prevention and treatment of autoimmune thrombocytopaenic purpura
XX and also for modulating binding of fibrinogen to thrombocytes
XX (particularly to dissolve thrombi and/or prevent their formation, e.g. in
XX cases of cardiac infarction or pulmonary embolism). Unlike murine
XX antibodies, human antibodies (hAb) do not induce adverse side effects and
XX persist for longer in vivo than small peptides
XX
XX Sequence 111 AA;
XX
Query Match 12.9%; Score 81.5; DB 2; Length 111;
Best Local Similarity 27.7%; Pred. No. 0.59;
Matches 33; Conservative 14; Mismatches 47; Indels 25; Gaps 6;
XX
QY 3 VSQPEIRTLGGSAFLPCSFNASQGRLAGSVTWFRDEVVPGKEVR-----NGT 52
Db 2 VTQPPESAGTFCQWVTISCS--GSSNIRNPNFVSMYHQ--VFGTAPKLLIFGSHQPSGV 57
XX
QY 53 PE-FEGRFLAPLASSRFLHDHQAELHIRDVGRGHDASIYVCRVEVLGL-GVGTGNGTRLVW 109
Db 58 PDRFSGSXSCTAS-----LAIRGLQSGDAGDYCATWDDGLNGPVGSGTKLV 107
XX

```

RESULT 13

AAV68807
ID AAV68807 standard; protein; 111 AA.

AC AAV68807;
XX

DT 16-MAY-2000 (first entry)

XX A light chain variable region of a rat anti-CD3 IgG antibody.

DE CD3 antigen complex; chimeric antibody; immunosuppression; light chain;
KW CD3 antigen-T-cell receptor complex; graft rejection; cancer.

XX Rattus sp.
OS

XX WO200005268-A1.
FN

XX 03-FEB-2000.
PD

XX 21-JUL-1999; 99WO-GB002380.
PF

XX 21-JUL-1998; 98GB-00015909.
PR

XX (BTGI-) BTG INT LTD.
PA

XX Waldmann H, Frewin M;
PI

XX WPI; 2000-182655/16.
DR

XX N-PSDB; AAZ60596.
DR

XX New humanized anti-CD3 antibodies, used for treating cancer or for
PT immunosuppression and preventing graft rejection.

XX Claim 5; Page 40-41; 56pp; English.
PS

XX The present sequence represents the light chain variable region of a rat
CC immunoglobulin G (IgG) antibody which is specific for the CD3 antigen
CC complex. The light chain variable regions is used to produce chimeric
CC human/rodent anti-CD3 antibodies, which have a rodent CD3 light chain
CC variable region and a human heavy chain variable region. The anti-CD3
CC antibodies can render T-cells non-functional by antibody blockade of the
CC CD3 antigen-T-cell receptor (TCR) complex. They can be used for
CC immunosuppression, particularly for the control of graft rejection. The
CC antibodies can also enhance or re-direct T-cell responses to antigens.
CC They can be used in the treatment of cancer
XX

SQ Sequence 111 AA;

Query Match 12.9%; Score 81.5; DB 3; Length 111;

Best Local Similarity 26.4%; Pred. No. 0.59;

Matches 32; Conservative 16; Mismatches 44; Indels 29; Gaps 6;

QY 3 VSQPPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFR-----DEWVPGKEVR 49

Db 4 VTQANSVSTSLGTVKLSCTL--SSGNIENNVYHVYQLYEGRSPTMIYDDKRP----- 56

QY 50 NGTPE-FRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLVGVTGNGTRLV 108

Db 57 DGVDFRFGSIDRSSNSAFLLTHNVAI-----EDEALYFCHSYVSSFNV-FGGGTKLT 108

QY 109 V 109

Db 109 V 109

RESULT 14

AAW41406
ID AAW41406 standard; protein; 120 AA.

XX AAW41406;
AC

XX 17-OCT-2003 (revised)
DT

DT 02-JUN-1998 (first entry)

XX Humanised antibody 806.077 HuVH6 chain.

XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region; Fd chain.

XX Homo sapiens.
OS

XX Mus sp.
OS

XX Chimeric.
OS

XX WO9742329-A1.
PN

XX 13-NOV-1997.
PD

XX 29-APR-1997; 97WO-GB001165.
PF

XX 04-MAY-1996; 96GB-00009405.
PR

XX 14-FEB-1997; 97GB-00003103.
PR

XX (ZENE) ZENECA LTD.
PA

XX Copley CG, Edge MD, Emery SC;
PI

XX WPI; 1997-558987/51.
DR

XX N-PSDB; AAV17310.
DR

XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis
PT and therapy of cancer.

XX Example 12; Page 151-152; 208pp; English.
PS

XX This sequence is the HuVH6 region of the antibody of the invention. The
CC antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab).
CC Host cells or transgenic organisms transformed with DNA encoding the
CC antibody, are used to make the antibody or conjugate. The conjugate is
CC used in a medicament suitable for intravenous administration. The
CC conjugate can be used for cancer therapy, selectively killing tumour
CC cells. The antibody can be used for in vivo or in vitro diagnosis of
CC cancer. (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 120 AA;

Query Match 12.9%; Score 81.5; DB 2; Length 120;

Best Local Similarity 27.0%; Pred. No. 0.66;

Matches 31; Conservative 10; Mismatches 35; Indels 39; Gaps 6;

QY 2 WVSQPPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFRDVEVPGKEVRNG----TPEFRG 57

Db 36 WVRQPP-----GR-GLEWIGWIDPE-----NGDTYAPKFRG 66

QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLVGVT---GNGTRLV 109

Db 67 RATWLADS---SKNQASRLSSVTAADTAIVYCHVLIYAGYLAMDYWGQGLTVTV 118

RESULT 15

ABR54951

ID ABR54951 standard; protein; 110 AA.

XX ABR54951;
AC

XX 30-JUN-2003 (first entry)
DT

XX IgG light chain clone HBL5 3D1 SEQ ID NO:177.
DE

XX Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.

XX Homo sapiens.
OS

XX Synthetic.
OS

XX WO2003025202-A2.
FN

	Query Match	12.7%; Score 80.5; DB 6; Length 110;
	Best Local Similarity	26.4%; Pred. NO. 0.76;
	Matches	32; Conservative 18; Mismatches 40; Indels 31; Gaps 6;
Qy	3 VSQPPEIRTLGSSAFLPCSFNASQGRIAGSVTWRFDEVVPGK-----EVANGT	52
Dd	6 LTQPSPVSVAFCQTARITCGNS----IGSKSVHWYQQ--PGAPVLVWVDSDRPSGI	59
Qy	53 PEFRGRPLAPSRLFHDHQ---AEHLHIRDVRGHDASTIVCRV-EVLGLGVGTGNTRLV	108
Dd	60 PE-----RFGSNSGTTALTISRVEAGDEADYYCQWDSTDQRVVFGGTKLT	108
Qy	109 V 109	
Dd	109 V 109	

Search completed: November 16, 2004, 23:39:44
Job time : 154 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 23:43:07 ; Search time 138 Seconds
(without alignments)
307.669 Million cell updates/sec

Title: US-10-036-444-4
Perfect score: 632
Sequence: 1 LWSQPPPIRTLEGGSAFLP.....TNGTRLVVEKEHPOLGAGT 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 769785

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/prodata1/pubaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/prodata1/pubaa/US07_PUB_PUB.pcp.*
3: /cgn2_6/prodata1/pubaa/US06_PUBCOMB.pcp.*
4: /cgn2_6/prodata1/pubaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/prodata1/pubaa/US07_PUB_PUB.pcp.*
6: /cgn2_6/prodata1/pubaa/US07_PUBCOMB.pcp.*
7: /cgn2_6/prodata1/pubaa/US08_PUB_PUB.pcp.*
8: /cgn2_6/prodata1/pubaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/prodata1/pubaa/US09_PUBCOMB.pcp.*
10: /cgn2_6/prodata1/pubaa/US09_PUBCOMB.pcp.*
11: /cgn2_6/prodata1/pubaa/US09_PUBCOMB.pcp.*
12: /cgn2_6/prodata1/pubaa/US09_PUBCOMB.pcp.*
13: /cgn2_6/prodata1/pubaa/US10_PUBCOMB.pcp.*
14: /cgn2_6/prodata1/pubaa/US10_PUBCOMB.pcp.*
15: /cgn2_6/prodata1/pubaa/US10_PUBCOMB.pcp.*
16: /cgn2_6/prodata1/pubaa/US10_PUBCOMB.pcp.*
17: /cgn2_6/prodata1/pubaa/US10_PUB_PUB.pcp.*
18: /cgn2_6/prodata1/pubaa/US11_PUB_PUB.pcp.*
19: /cgn2_6/prodata1/pubaa/US11_PUB_PUB.pcp.*
20: /cgn2_6/prodata1/pubaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	632	100.0	120	13	US-10-036-444-4
2	89.5	14.2	110	14	US-10-269-805-50
3	87.5	13.8	115	14	US-10-029-386-32704
4	85.5	13.5	109	14	US-10-001-934-44
5	85.5	13.5	109	15	US-10-275-046-75
6	85.5	13.5	120	9	US-09-910-059-81
7	84.5	13.4	108	10	US-09-791-153A-74
8	84.5	13.4	110	14	US-10-371-942-44
9	83.5	13.2	120	9	US-09-910-059-79
10	83.5	13.2	120	9	US-09-910-059-91
11	81.5	12.9	111	9	US-09-736-371B-15
12	81.5	12.9	111	15	US-10-463-442-15
13	81.5	12.9	111	17	US-10-844-424-4

14	81.5	12.9	120	9	US-09-910-059-89	Sequence 89, Appl
15	80.5	12.7	110	15	US-10-251-085B-177	Sequence 177, Appl
16	80.5	12.7	110	16	US-10-737-252-177	Sequence 177, Appl
17	79.5	12.6	109	15	US-10-275-046-77	Sequence 77, Appl
18	78.5	12.4	110	14	US-10-269-805-60	Sequence 60, Appl
19	78.5	12.4	110	15	US-10-251-085B-166	Sequence 166, Appl
20	78.5	12.4	110	16	US-10-723-434-52	Sequence 52, Appl
21	78.5	12.4	110	16	US-10-737-252-166	Sequence 166, Appl
22	78	12.3	95	15	US-10-424-593-200781	Sequence 200781, Appl
23	78	12.3	107	10	US-09-913-238-67	Sequence 67, Appl
24	77.5	12.3	110	16	US-10-723-434-48	Sequence 48, Appl
25	77.5	12.3	116	16	US-10-684-109-39	Sequence 39, Appl
26	77	12.2	116	15	US-10-269-711-3	Sequence 3, Appl
27	77	12.2	116	16	US-10-684-109-3	Sequence 3, Appl
28	76.5	12.1	109	14	US-10-001-934-52	Sequence 52, Appl
29	76.5	12.1	109	15	US-10-275-046-91	Sequence 91, Appl
30	76.5	12.1	110	15	US-10-251-085B-163	Sequence 163, Appl
31	76.5	12.1	110	16	US-10-737-252-163	Sequence 163, Appl
32	76.5	12.1	112	16	US-10-779-461-143	Sequence 143, Appl
33	76.5	12.1	120	9	US-09-910-059-75	Sequence 75, Appl
34	76	12.0	15	13	US-10-036-444-7	Sequence 7, Appl
35	75.5	11.9	103	10	US-09-848-798-180	Sequence 180, Appl
36	75.5	11.9	109	14	US-10-001-934-50	Sequence 50, Appl
37	75.5	11.9	109	15	US-10-275-046-79	Sequence 79, Appl
38	75.5	11.9	109	15	US-10-275-046-89	Sequence 89, Appl
39	75.5	11.9	110	14	US-10-447-331-1	Sequence 1, Appl
40	75.5	11.9	110	15	US-10-251-085B-170	Sequence 170, Appl
41	75.5	11.9	110	16	US-10-737-252-170	Sequence 170, Appl
42	75	11.9	110	15	US-10-251-085B-173	Sequence 173, Appl
43	75	11.9	110	16	US-10-737-252-173	Sequence 173, Appl
44	75	11.9	111	14	US-10-091-300-35	Sequence 35, Appl
45	75	11.9	116	16	US-10-684-109-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-036-444-4
; Sequence 4, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PE-1060
; CURRENT APPLICATION NUMBER: US/10/036.444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-4

Query Match	100.0%	Score	632	DB	13	Length	120
Best Local Similarity	100.0%	Pred. No.	3.2e-61	Indels	0	Gaps	0
Matches	120	Conservative	0	Mismatches	0		
QY	1	LWSQPPPIRTLEGGSAFLP	CSFNASQGRLAIGSVTWF	FRDEVPFGKEVNRNGT	PEFRGLA	60	
Db	1	LWSQPPPIRTLEGGSAFLP	CSFNASQGRLAIGSVTWF	FRDEVPFGKEVNRNGT	PEFRGLA	60	
QY	61	PLASRFHLDHQAEHLHIDVRGHDAS	IYVCREVGLGVGTGNGTR	LVVEKEHPOLGAGT	120		
Db	61	PLASRFHLDHQAEHLHIDVRGHDAS	IYVCREVGLGVGTGNGTR	LVVEKEHPOLGAGT	120		

```
RESULT 2
US-10-269-805-50
; Sequence 50, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-50

Query Match          14.2%; Score 89.5; DB 14; Length 110;
Best Local Similarity 26.3%; Pred. No. 0.084; Indels 23; Gaps 6;
Matches 31; Conservative 20; Mismatches 44;

QY 3 VSQPPERTLEGSAFLPCSFNASQGRLAIGSVTWFRDEVVPG-----KEVRNGT 52
DB 4 LTQPHSVSESPGKTVIIPCT--RSSGSIASNYQWYQKR--PGSAPSIVIVEDKQRP 59
QY 53 PE-FRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVLGLVGTGNGTRLV 109
DB 60 PDRFSGSIDSSNS-----ASLTISGLKTEADYICQ--SYNRRGVWFGGKTLTV 109

RESULT 3
US-10-029-386-32704
; Sequence 32704, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32704
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050328.24
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.65
; OTHER INFORMATION: SWISSPROT HIT: Q16653, EVALUE 3.00e-64
US-10-029-386-32704

Query Match          13.8%; Score 87.5; DB 14; Length 115;
Best Local Similarity 34.0%; Pred. No. 0.15; Indels 19; Gaps 6;
Matches 32; Conservative 9; Mismatches 34;

QY 9 IRTLEGSAFLPCSFNASQGRLAIG-SVTWFRDEVVPGKEV-----RNG-----TPEFR 56
DB 11 IRLAVGDEVELPC--RISPGKATGMVGVWYRP--PFSRVVHLYRNGKQDQDQAEYR 65
QY 57 GLRLAPLASSRFLHDHQAELHIRDVGRGHDAIYVC 90
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```
DB 66 GRTELLXDA--IGEGKVTLRINVRPDSDEGGFTC 97

RESULT 4
US-10-001-934-44
; Sequence 44, Application US/10001934
; Publication No. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: NAGY, ZOLTAN
; TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
; FILE REFERENCE: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
; FILE REFERENCE: GFCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/001,934
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 44
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-44

Query Match          13.5%; Score 85.5; DB 14; Length 109;
Best Local Similarity 26.7%; Pred. No. 0.23; Indels 29; Gaps 7;
Matches 32; Conservative 22; Mismatches 37;

QY 3 VSQPPERTLEGSAFLPCSFNASQGRLAIGS--VTWFRDEVVPGKEVR-----N 50
DB 4 LTQPPSVSGAPGQRTVISCSSSN---IGSNVSVWYQQ--LPGTAPKLLIYDNNQRP 57
QY 51 GTPE-FRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVLGLVGTGNGTRLV 109
DB 58 GVDPFRFSGSKSGTSAS-----LAITGLQSEADYICQSYDLTMGV-FGGGKTLTV 107

RESULT 5
US-10-275-046-75
; Sequence 75, Application US/10275046
; Publication No. US20040019187A1
; GENERAL INFORMATION:
; APPLICANT: Nagy et al.
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275,046
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MS-GPC10 VL
US-10-275-046-75

Query Match          13.5%; Score 85.5; DB 15; Length 109;
Best Local Similarity 26.7%; Pred. No. 0.23; Indels 29; Gaps 7;
Matches 32; Conservative 22; Mismatches 37;

QY 3 VSQPPERTLEGSAFLPCSFNASQGRLAIGS--VTWFRDEVVPGKEVR-----N 50
DB 4 LTQPPSVSGAPGQRTVISCSSSN---IGSNVSVWYQQ--LPGTAPKLLIYDNNQRP 57
QY 51 GTPE-FRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVLGLVGTGNGTRLV 109
DB 58 GVDPFRFSGSKSGTSAS-----LAITGLQSEADYICQSYDLTMGV-FGGGKTLTV 107

RESULT 6
US-09-910-059-81
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; Sequence 81, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 81
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised heavy chain variable region variant
US-09-910-059-81

Query Match      13.5%; Score 85.5; DB 9; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.26;
Matches 31; Conservative 11; Mismatches 34; Indels 39; Gaps 6;

QY 2 WVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG-----TFEPRG 57
Db 36 WVRQPP-----GR-GLEWIAWIDPE-----NGDTEYAPKFRG 66
QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVVEVLGLGVGT 109
Db 67 RVTWLADS-----SKNQASLRSSVTADTAVYCHVLIYAGYLANDYWGQGLTVV 118

RESULT 7
US-09-791-153A-74
; Sequence 74, Application US/09791153A
; Patent No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 74
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-74

Query Match      13.4%; Score 84.5; DB 10; Length 108;
Best Local Similarity 29.4%; Pred. No. 0.29;
Matches 35; Conservative 17; Mismatches 40; Indels 27; Gaps 7;

QY 3 VSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGK-----EVRNGT 52
Db 4 LTQPPSVSAAPGQIVTISCS--GSSNIGRNVYVWFQ--VPGRAPKLLIYDNNQRPSGI 57

; Sequence 81, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 81
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised heavy chain variable region variant
US-09-910-059-81

Query Match      13.5%; Score 85.5; DB 9; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.26;
Matches 31; Conservative 11; Mismatches 34; Indels 39; Gaps 6;

QY 2 WVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG-----TFEPRG 57
Db 36 WVRQPP-----GR-GLEWIAWIDPE-----NGDTEYAPKFRG 66
QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVVEVLGLGVGT 109
Db 67 RVTWLADS-----SKNQASLRSSVTADTAVYCHVLIYAGYLANDYWGQGLTVV 118

RESULT 7
US-09-791-153A-74
; Sequence 74, Application US/09791153A
; Patent No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 74
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-74

Query Match      13.4%; Score 84.5; DB 10; Length 108;
Best Local Similarity 29.4%; Pred. No. 0.29;
Matches 35; Conservative 17; Mismatches 40; Indels 27; Gaps 7;

QY 3 VSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGK-----EVRNGT 52
Db 4 LTQPPSVSAAPGQIVTISCS--GSSNIGRNVYVWFQ--VPGRAPKLLIYDNNQRPSGI 57
```

```
QY 53 PE-FRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVVEVLGLGVGTGNGTRLVW 109
Db 58 PERFSG-----SSS-----GTEVTLISGVQAEDADYVCSQSDSSGTYVVFVGSGTKLTV 107

RESULT 8
US-10-371-942-44
; Sequence 44, Application US/10371942
; Patent No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Voram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-44

Query Match      13.4%; Score 84.5; DB 14; Length 110;
Best Local Similarity 26.9%; Pred. No. 0.3;
Matches 32; Conservative 17; Mismatches 45; Indels 25; Gaps 7;

QY 3 VSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGKEVR-----NGT 52
Db 4 LTQPPSVSAAPGQIVTISCS--GSSNIGRNVYVWFQ--VPGRAPKLLIYDNNQRPSGI 59
QY 53 PEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRV--EVLGLGVGTGNGTRLVW 109
Db 60 P---GRFSASKS-----DTSATLDTITGLQSGDEAVYVCGTWDSTLDLVV-FGGGTHVTV 109
```

```
RESULT 9
US-09-910-059-79
; Sequence 79, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 79
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised heavy chain variable region variant
US-09-910-059-79

Query Match      13.2%; Score 83.5; DB 9; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.43;
Matches 31; Conservative 11; Mismatches 34; Indels 39; Gaps 6;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 23:34:26 ; Search time 39 Seconds
(without alignments)
204.055 Million cell updates/sec

Title: US-10-036-444-4
Perfect score: 632
Sequence: 1 LWSQPPETRTLEGGSAFLP.....TGNGLVVEKEHPQLGAGT 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 327303

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/prodata/1/iaa/PCITUS COMB.pcp.*
6: /cgn2_6/prodata/1/iaa/backfilesl.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89.5	14.2	120	3	US-09-171-945-89
2	87.5	13.8	120	4	US-09-472-087-102
3	85.5	13.5	120	3	US-09-171-945-81
4	83.5	13.2	120	3	US-09-171-945-79
5	83.5	13.2	120	3	US-09-171-945-91
6	81.5	12.9	110	2	US-08-362-780-26
7	81.5	12.9	111	4	US-09-424-840-4
8	79.5	12.6	109	3	US-09-157-370-5
9	77.5	12.3	109	3	US-09-460-384-34
10	76.5	12.1	120	3	US-09-171-945-75
11	75.5	11.9	109	3	US-09-240-274-180
12	75.5	11.9	120	2	US-08-428-197-13
13	75.5	11.9	120	5	PCT-US93-10555-13
14	75	11.9	108	3	US-09-025-769B-20
15	75	11.9	108	4	US-09-490-070A-20
16	75	11.9	108	4	US-09-490-153-20
17	74.5	11.8	112	4	US-09-025-769B-18
18	74.5	11.8	112	4	US-09-490-070A-18
19	74.5	11.8	112	4	US-09-490-153-18
20	74.5	11.8	120	3	US-09-171-945-55
21	74	11.7	92	3	US-08-928-383B-15
22	74	11.7	108	3	US-09-240-274-68
23	73	11.6	112	2	US-08-565-202-39
24	73	11.6	112	4	US-08-315-574-39
25	72.5	11.5	111	2	US-08-865-202-41
26	72.5	11.5	111	4	US-09-315-574-41
27	72.5	11.5	120	3	US-09-171-945-85

28	72	11.4	93	2	US-08-341-843B-8	Sequence 8, Appli
29	72	11.4	93	2	US-08-427-497E-13	Sequence 13, Appli
30	72	11.4	112	3	US-09-240-274-64	Sequence 64, Appli
31	71.5	11.3	109	3	US-09-202-181-2	Sequence 2, Appli
32	71.5	11.3	109	3	US-09-240-274-56	Sequence 56, Appli
33	71.5	11.3	109	3	US-09-025-769B-32	Sequence 32, Appli
34	71.5	11.3	109	3	US-09-025-769B-51	Sequence 51, Appli
35	71.5	11.3	109	4	US-09-480-070A-32	Sequence 32, Appli
36	71.5	11.3	109	4	US-09-490-070A-51	Sequence 51, Appli
37	71.5	11.3	109	4	US-09-490-153-32	Sequence 32, Appli
38	71.5	11.3	109	4	US-09-490-153-51	Sequence 51, Appli
39	71.5	11.3	110	1	US-07-988-925-16	Sequence 16, Appli
40	71.5	11.3	110	2	US-08-362-780-16	Sequence 16, Appli
41	71.5	11.3	110	4	US-08-478-684G-16	Sequence 16, Appli
42	71	11.2	105	1	US-08-488-113B-157	Sequence 157, App
43	71	11.2	105	1	US-08-477-484B-157	Sequence 157, App
44	71	11.2	105	1	US-08-107-669D-21	Sequence 21, Appl
45	71	11.2	105	1	US-08-472-788A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-171-945-89
; Sequence 89, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 89
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-89

Query Match	14.2%	Score 89.5;	DB 3;	Length 120;
Best Local Similarity	27.8%	Pred. No. 0.01;		
Matches	32;	Conservative	10;	Mismatches 34;
				Indels 39;
				Gaps 6;
QY	2	WVSQPPETRTLEGGSAFLP	CSFNASQGR	LAIGSVTFRDEVVPGKEVRNG-----TPPFRG 57
Db	36	WVRQPP-----	GR-GLGWIGWIDPE-----	NGDTEYAPKFRG 66
QY	58	RLAPLASSRFLHQAEHLHVRGHDASIVVCRVVLGLGVGT---	GNGTRLVV 109	
Db	67	RATMLADS---	SKNQASRLSSVTADTAVYCHVLIYAGYLANDYWGQGLTVTV 118	

RESULT 2
US-09-472-087-102
; Sequence 102, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.

```

; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-472-087-102

Query Match          13.8%; Score 87.5; DB 4; Length 120;
Best Local Similarity 27.4%; Pred. No. 0.017;
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;

QY 3 VSOQPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPL 62
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 VAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTLRQADSVTEVCAATYMWGNELT-- 59
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ASGRFLHD-----HQAEHLHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRLVVE 110
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 ----FLDDSICTGSSGNQVNLTIQGLRMDTGLYCKVELMYPPIYLGNGTQIYVI 115
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 KEHP 114
   |
Db 116 DPEP 119

RESULT 3
US-09-171-945-81
; Sequence 81, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-81

Query Match          13.5%; Score 85.5; DB 3; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.03;
Matches 31; Conservative 11; Mismatches 34; Indels 39; Gaps 6;

QY 2 VWSQPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG----TPEFRG 57
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 WVRQPP-----GR-GLEWIAIDPE-----NGDTEYAPKFRG 66
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 RLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGT---GNGTRLVV 109
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 RVTWLADS-----SKQASRLSSVTADTAVTYCHVLIYAGYLANDYWGQTLVTV 118
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-171-945-91
; Sequence 91, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-91

Query Match          13.2%; Score 83.5; DB 3; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.05;
Matches 31; Conservative 11; Mismatches 34; Indels 39; Gaps 6;

QY 2 VWSQPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG----TPEFRG 57
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 WVRQPP-----GR-GLEWIAIDPE-----NGDTEYAPKFRG 66
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 RLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGT---GNGTRLVV 109
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 RVTWLADS-----SKQASRLSSVTADTAVTYCHVLIYAGYLANDYWGQTLVTV 118
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
US-09-171-945-79
; Sequence 79, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-79

Query Match          13.2%; Score 83.5; DB 3; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.05;
Matches 31; Conservative 11; Mismatches 34; Indels 39; Gaps 6;

QY 2 VWSQPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG----TPEFRG 57
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 WVRQPP-----GR-GLEWIAIDPE-----NGDTEYAPKFRG 66
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 RLAPLASSRFLHDHQAEHLHIRDVRGHDASIYVCRVEVLGLGVGT---GNGTRLVV 109
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 RVTWLADS-----SKQASRLSSVTADTAVTYCHVLIYAGYLANDYWGQTLVTV 118
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-09-171-945-91
; Sequence 91, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-91
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US-09-171-945-91

Query Match 13.2%; Score 83.5; DB 3; Length 120;
Best Local Similarity 27.0%; Pred. No. 0.05; 35; Indels 39; Gaps 6;
Matches 31; Conservative 10; Mismatches 35; Indels 39; Gaps 6;

QY 2 WVSQPEIRTEGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG---TPEFRG 57

Db 36 WVRQPP-----GR-GLEIAWIDPE-----NGDTEYAPKFRG 66

QY 58 RLAPLASSRFLHDHQRHLDVGRGHDASIVYCRVEVLGLGVGT---GNGTRLVV 109

Db 67 RATMLADS-----SKNQASLRUSSVTRADTAVYCHVLIYAGYLANDYWGQGLTVV 118

RESULT 6

US-08-362-780-26

; Sequence 26, Application US/08362780

; Patent No. 5968509

; GENERAL INFORMATION:

; APPLICANT: Gorman, Scott D

; APPLICANT: Routledge, Edward G

; APPLICANT: Walldmann, Herman

; TITLE OF INVENTION: Antibody Preparation

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon and Vanderhye pc

; STREET: 8th Floor, 1100 No. 5968509th Glebe Road

; CITY: Arlington

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08362,780

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/862,543

; FILING DATE: 23-JUNE-1992

; APPLICATION NUMBER: GB 9021679.7

; FILING DATE: 05-OCT-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB91/01726

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Mitchard, Leonard C

; REGISTRATION NUMBER: 29009

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 7038164000

; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 110 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-362-780-26

Query Match 12.9%; Score 81.5; DB 2; Length 110;

Best Local Similarity 26.4%; Pred. No. 0.076;

Matches 32; Conservative 16; Mismatches 44; Indels 29; Gaps 6;

QY 3 VVSQPEIRTEGSAFLPCSFNASQGRLAIGSVTWFR-----DEVVPGKEVR 49

Db 4 VTQANSVSTSLGIVKLSCTL--SSGNIENNVYVWYQVGRGPTTWIYDDKRP----- 56

QY 50 NGTPE-FRGLAPLASSRFLHDHQRHLDVGRGHDASIVYCRVEVLGLGVGTGNGTRLV 108

Db 57 DGVDFRSGSIDRSSNAFLTIHVAI-----EDEALYFCHSYVSSFNV-FGGTKLT 108

QY 109 V 109

Db 109 V 109

RESULT 7

US-09-424-840-4

; Sequence 4, Application US/09424840

; Patent No. 6790938

; GENERAL INFORMATION:

; APPLICANT: BERCHTOLD, Peter

; APPLICANT: ESCHER, Robert F.A.

; TITLE OF INVENTION: Anti-GPIIb/IIIa Recombinant Antibodies

; FILE REFERENCE: 100564-09049

; CURRENT APPLICATION NUMBER: US/09/424,840

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: DE 19723904.8

; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: DE 19755227.7

; PRIOR FILING DATE: 1997-12-12

; PRIOR APPLICATION NUMBER: DE 19820663.1

; PRIOR FILING DATE: 1998-05-08

; NUMBER OF SEQ ID NOS: 127

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 4

; LENGTH: 111

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-424-840-4

Query Match 12.9%; Score 81.5; DB 4; Length 111;

Best Local Similarity 27.7%; Pred. No. 0.077;

Matches 33; Conservative 14; Mismatches 47; Indels 25; Gaps 6;

QY 3 VVSQPEIRTEGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVR-----NGT 52

Db 2 VTQPSASGTGQWVTSCS--GSSNIRSNPVSWYIQ--VPGTAPKLLIFGSHQRPSCV 57

QY 53 PE-FRGLAPLASSRFLHDHQRHLDVGRGHDASIVYCRVEVLGL-GVGTGNGTRLVV 109

Db 58 PDRFSGSKSGTAS-----LAIRGLQSGDAGDYVCATWDDGLNGPVGGGTKLTV 107

RESULT 8

US-09-157-370-5

; Sequence 5, Application US/09157370A

; Patent No. 6262238

; GENERAL INFORMATION:

; APPLICANT: STEIPE, Boris

; APPLICANT: STEINBACHER, Stefan

; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES

; FILE REFERENCE: P8341-8072

; CURRENT APPLICATION NUMBER: US/09/157,370A

; CURRENT FILING DATE: 1998-09-21

; EARLIER APPLICATION NUMBER: 08/765,179

; EARLIER FILING DATE: 1997-01-14

; EARLIER APPLICATION NUMBER: PCT/EP95/02626

; EARLIER FILING DATE: 1995-07-06

; EARLIER APPLICATION NUMBER: DE/P44 25 115.7

; EARLIER FILING DATE: 1994-07-15

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 5

; LENGTH: 109

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-157-370-5

Query Match 12.6%; Score 79.5; DB 3; Length 109;

Best Local Similarity 24.6%; Pred. No. 0.13;

Matches 29; Conservative 22; Mismatches 40; Indels 27; Gaps 6;

QY	3	V	S	P	O	P	E	I	R	T	L	E	S	S	A	F	L	P	C	S	F	N	S	O	G	R	L	A	I	G	S	V	T	W	F	R	D	E	V	P	G	K	E	V	R	-----NGT	52									
DB	4	L	T	P	O	P	E	V	S	V	P	G	T	V	T	I	S	C	S	G	S	-----L	G	I	G	H	V	S	W	I	Q	K	-	P	G	A	P	K	L	V	I	D	D	N	K	R	P	S	G	I	57					
QY	53	P	P	-	F	R	G	R	L	A	P	L	A	S	S	R	F	L	H	D	H	Q	E	L	H	I	R	D	V	R	G	H	D	A	S	I	Y	C	R	V	E	V	L	G	L	G	V	G	T	G	N	G	T	L	V	109
DB	58	P	R	F	G	S	G	S	-	-----	C	N	T	A	S	L	I	T	S	G	L	O	A	E	D	E	A	D	Y	C	O	-	S	W	D	S	S	S	V	V	F	G	G	T	K	L	V	105								

RESULT 9

```

US-09-460-384-34
; Sequence 34, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
; APPLICANT: EL TAYAR, Nabil
; BLECHNER, Steven
; JAMESON, Brad
; TEPPER, Mark
; TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
; PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
; SAME.
;

```

Query Match	12.3%;	Score 77.5;	DB 3;	Length 109;
Best Local Similarity	27.2%;	Pred. No. 0.22;		
Matches	31;	Conservative	13;	Mismatches 49;
				Indels 21;
				Gaps 4;

```

3  VQPEIRTLGSSAFPLPCSFNAGRIAGISVTFWRDEVPGKVRNGTTFEGRRLAPL 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3  VAQPAVLASSRGIAFSFCEY-ASPGKATEVRVTVLRQADSQVTECAATYMGNET-- 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 ASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL-----GLGVGTG 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
60 ----FLDISICTGSGNOVNTIQLRAMDTGLYICKVELMYPYPYVLGNG 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 10
US-09-171-945-75
; Sequence 75, Application US/09171945

```
Query Match      12.1%; Score 76.5; DB 3; Length 120;
Best Local Similarity    25.1%; Prd.No. 0.32;
Matches          29; Conservative   12; Mismatches   35; Indels       39; Gaps         6;
```

QY	2 WVSQPPIRTLEGSAPLPCSFNASOGRLAISGVTWFRDEVVPGKEVRNG-----TPPFRG 57
DB	36 WVROPP-----GR-GLEWIAMIDPE-----NGDTEVPKPRFG 66
QY	58 RLAPLASRFLHDHQALHIRDVRGHDSIIVCRVEVLGLGVGT---GNGLRLVV 109 :: : :: :
Db	67 RVTVIAQT--SKNPFSLRSSVTAAATVAIVYCHLVIIAGLYAMDWSOGILATV 118 :: : :: :

RESIST 11

```

US-09-240-274-180
; Sequence 180, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH55
US-09-240-274-180

```

Query Match 11.9%; Score 75.5; DB 3; Length 109;
Best Local Similarity 26.7%; Pred. No. 0.37;
Matches: 32: Conservative 16; Mismatches 45; Indels 27; Gaps 6;

4

```
Qy 3 VSQPEIRTLTGSSAFPLPCSNAGRLAIGS--VTWFRDEVVPGKEVR-----N 50
Db 3 LTQPPSASGTPGQRTVTCSSGSSN-----IGSKYVWYQQ--LPGTAPKLLIYNNQRPS 56
Qy 51 GTPEFRGLAPLASSRFLHDPHQAELHIRDVRGHDAIYVCRVEVLGL-GVGTGNGRLVV 109
Db 57 GVDP-----RFAFKSGTASLAITGLQAEDEANYCQSYDSGLSGWVFGGTKLTV 108

RESULT 12
US-08-428-197-13
; Sequence 13, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: KAS
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..120
US-08-428-197-13

Query Match 11.9%; Score 75.5; DB 2; Length 120;
Best Local Similarity 25.0%; Pred. No. 0.42;
Matches 29; Conservative 17; Mismatches 39; Indels 31; Gaps 6;

Qy 14 GSSAFPLPCSNAGRLAIGSVTWFRDEVVPGKEVR-----NGTPEFRGLAP 61
Db 14 GSSVKVSC--KASGTFSSYAISWVRQ--APGGGLEWMMGGIPIFGQANYAQKFGQRTVI 69
Qy 62 LASSRFLHQAELHIRDVRGHDAIYVCRVEVLGLGVGT-----GNGTRLVV 109
Db 70 TADE---STNTAYMELSLRSDDTAMYYCAKE---GYGDYGRPFDFWCGQLTVV 118

US-09-025-769B-20
; Sequence 20, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
```

```
RESULT 13
PCT-US93-10555-13
; Sequence 13, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: KAS
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..120
PCT-US93-10555-13

Query Match 11.9%; Score 75.5; DB 5; Length 120;
Best Local Similarity 25.0%; Pred. No. 0.42;
Matches 29; Conservative 17; Mismatches 39; Indels 31; Gaps 6;

Qy 14 GSSAFPLPCSNAGRLAIGSVTWFRDEVVPGKEVR-----NGTPEFRGLAP 61
Db 14 GSSVKVSC--KASGTFSSYAISWVRQ--APGGGLEWMMGGIPIFGQANYAQKFGQRTVI 69
Qy 62 LASSRFLHQAELHIRDVRGHDAIYVCRVEVLGLGVGT-----GNGTRLVV 109
Db 70 TADE---STNTAYMELSLRSDDTAMYYCAKE---GYGDYGRPFDFWCGQLTVV 118

RESULT 14
US-09-025-769B-20
; Sequence 20, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
```

CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: protein
MOLECULE TYPE: protein
US-09-025-769B-20

Query Match 11.9%; Score 75; DB 3; Length 108;
Best Local Similarity 24.6%; Pred. No. 0.42; Indels 26; Gaps 5;
Matches 29; Conservative 21; Mismatches 42; Indels 26; Gaps 5;
QY 3 VSQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFRDEVVPGK-----EVRNGT 52
DB 3 LTQPPSVVAPGQTARITCSGDSLGSKYA---SWYQK--PGQAPVLVIYDDNKRPSGI 56
QY 53 PE-FRGLAPLASSRFLHDAQELHIRDVRGHDAIYVCRVEVLGLGVGTGNGTRLV 109
DB 57 PERFGSGNS-----GNTATLTISGVAEDEADYICQSWDSSGNVVFVGGTKLT 105

RESULT 15
US-09-430-070A-20
Sequence 20, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (BFO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-490-070A-20
Query Match 11.9%; Score 75; DB 4; Length 108;
Best Local Similarity 24.6%; Pred. No. 0.42; Indels 26; Gaps 5;
Matches 29; Conservative 21; Mismatches 42; Indels 26; Gaps 5;
QY 3 VSQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFRDEVVPGK-----EVRNGT 52
DB 3 LTQPPSVVAPGQTARITCSGDSLGSKYA---SWYQK--PGQAPVLVIYDDNKRPSGI 56
QY 53 PE-FRGLAPLASSRFLHDAQELHIRDVRGHDAIYVCRVEVLGLGVGTGNGTRLV 109
DB 57 PERFGSGNS-----GNTATLTISGVAEDEADYICQSWDSSGNVVFVGGTKLT 105
Search completed: November 16, 2004, 23:43:46
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 23:17:04 ; Search time 38 Seconds
(without alignments)
48.108 Million cell updates/sec

Title: US-10-036-444-5
Perfect score: 88
Sequence: 1 VLLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 3436

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	38.6	16	2	Ti4224
2	28	31.8	10	1	ECLQ3M
3	28	31.8	11	2	PH1632
4	27	30.7	11	1	ECLQ2M
5	24	27.3	10	1	ECLQ1M
6	24	27.3	13	2	PH0787
7	24	27.3	14	2	B61597
8	24	27.3	15	2	PA0046
9	23	26.1	16	2	S11290
10	23	26.1	19	2	B60822
11	22	25.0	10	2	PQ0784
12	22	25.0	11	2	D41946
13	22	25.0	18	2	B44395
14	22	25.0	19	2	PH1360
15	22	25.0	19	2	A39504
16	21.5	24.4	12	2	PH1506
17	21	23.9	10	2	S06964
18	21	23.9	11	2	S53436
19	21	23.9	12	2	PN0162
20	21	23.9	15	2	A61322
21	21	23.9	16	2	PH1580
22	20	22.7	13	2	S36874
23	20	22.7	13	2	PH1596
24	20	22.7	14	2	A60770
25	20	22.7	15	2	A49252
26	20	22.7	15	2	PH1616
27	20	22.7	16	2	C49048
28	20	22.7	16	2	S09732
29	20	22.7	16	2	A59155

30 20 22.7 17 2 H49048 T-cell receptor be
31 20 22.7 17 2 I49048 T-cell receptor be
32 20 22.7 17 2 S77901 methylitaconate De
33 20 22.7 18 2 B49048 T-cell receptor be
34 20 22.7 19 2 G49048 T-cell receptor be
35 20 22.7 19 2 PH1755 T-cell receptor al
36 20 22.7 19 2 E49048 T-cell receptor be
37 19 21.6 11 2 S33782 acetolactate synth
38 19 21.6 11 2 S23364 T-cell receptor al
39 19 21.6 12 2 S34447 binr protein - Sta
40 19 21.6 12 2 PH1587 IG H chain V-D-J r
41 19 21.6 13 2 PT0304 IG heavy chain CRD
42 19 21.6 13 2 PH0805 T-cell receptor al
43 19 21.6 14 2 A33798 D-amino-acid oxida
44 19 21.6 14 2 PT0252 IG heavy chain CRD
45 19 21.6 14 2 PC4376 telomeric and tetr

ALIGNMENTS

RESULT 1

Ti4224

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Euhadra herklotsi mitochondrion
C:Species: mitochondrion Euhadra herklotsi

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: Ti4224

R.Yamazaki, N.; Ueshima, R.; Terrett, J.A.; Yokobori, S.; Kaifu, M.; Segawa, R.; Kobaya
submitted to the EMBL Data Library, May 1996

A:Description: Evolution of pulmonate gastropod mitochondrial genomes: Comparisons of c

A:Reference number: Z17932

A:Accession: Ti4224

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Restrictions: 1-16 <YAM>

A:Cross-references: UNIPROT:P92070; EMBL:Z71694; NID:e912660; PID:e244560; PIDN:CAA9636

A:Experimental source: adult; hepatopancreas

C:Genetics:

A:Genome: mitochondrion

C:Keywords: mitochondrion; NAD; oxidoreductase

Query Match 38.6%; Score 34; DB 2; Length 16;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 FYAVSFLSVAV 18

DB 5 FYVMSFLLVGV 15

RESULT 2

ECLQ3M

tachykinin III - migratory locust

N:Alternate names: locustatachykinin III

C:Species: Locusta migratoria (migratory locust)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C:Accession: A60073

R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Kochansky, J.P.; Nachman, R.J.; De Loof, A.

Regul. Pept. 31, 199-212, 1990

A:Title: Locustatachykinin III and IV: two additional insect neuropeptides with homology

A:Reference number: A60073; MUID:91219696; PMID:2132575

A:Accession: A60073

A:Molecule type: protein

A:Residues: 1-10 <SCH>

A:Cross-references: UNIPROT:P30249

C:Superfamily: tachykinin

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

P:10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 31.8%; Score 28; DB 1; Length 10;

Best Local Similarity 71.4%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 RAGFYAV 11
:|||||
Db 3 QAGFYGV 9

RESULT 3

PH1632
Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1632
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1632
A:Molecule type: DNA
A:Residues: 1-11 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 31.8%; Score 28; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 RAGFYAVSF 13
:|||||
Db 3 RRGYAMDY 11

RESULT 4

ECLOQM
tachykinin II - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S08266
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
FEBS Lett. 261, 397-401, 1990
A:Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to pep
A:Reference number: S08265; MUID:90184489; PMID:2311766
A:Accession: S08266
A:Molecule type: protein
A:Residues: 1-11 <SCH>
A:Cross-references: UNIPROT:P16224
C:Superfamily: tachykinin
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 30.7%; Score 27; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LRAGFYAV 11
:|||||
Db 3 LSSGFYGV 10

RESULT 5

ECLOQM
tachykinin I - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S08265
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
FEBS Lett. 261, 397-401, 1990
A:Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to pep
A:Reference number: S08265; MUID:90184489; PMID:2311766
A:Accession: S08265
A:Molecule type: protein
A:Residues: 1-10 <SCH>
A:Cross-references: UNIPROT:P16223
C:Superfamily: tachykinin

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 27.3%; Score 24; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGFYAV 11
:|||||
Db 4 SGFYGV 9

RESULT 6

PH0787
T-cell receptor alpha chain (F8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0787
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-I
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078845; PMID:1836010
A:Accession: PH0787
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60891
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 27.3%; Score 24; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLRAGF 8
:|||||
Db 2 LLRAGY 7

RESULT 7

B61597
cytochrome P450 AL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: B61597
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cytochr
A:Reference number: A61597; MUID:91292910; PMID:1676625
A:Accession: B61597
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHI>
A:Cross-references: UNIPROT:Q7M047

Query Match 27.3%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LLRAGFYAVSF 13
:|||||
Db 3 LLLSLFLVGF 14

RESULT 8

PA0046
protein QA00044 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0046; PA0042
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JFPD, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona

A:Reference number: PA0001
 A:Accession: PA0046
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: stem

Query Match 27.3%; Score 24; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 RAGFYAVS 12
 :|||
 Db 4 KKGFLAVS 11

RESULT 9

S11290
 matrix protein M1 - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)
 C:Species: influenza A virus
 C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C:Accession: S11290
 R:Robertson, J.S.
 Nucleic Acids Res. 6, 3745-3757, 1979
 A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza A
 A:Reference number: S11286; MUID:80034428; PMID:493121
 A:Accession: S11290
 A:Molecule type: genomic RNA
 A:Residues: 1-16 <ROB>
 A:Cross-references: UNIPROT:Q84098; EMBL:J02112
 C:Genetics:
 A:Map position: segment 7
 C:Superfamily: influenza virus matrix protein M1

Query Match 26.1%; Score 23; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 1.9e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 LLRAGFYAVS 12
 :|||
 Db 3 LLTEVGTYVLS 13

RESULT 10

B60822
 cytochrome P450 UT50 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
 C:Accession: B60822
 R:Ameliazad, Z.; Marbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.
 Biochem. Pharmacol. 37, 3245-3249, 1988
 A:Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.
 A:Reference number: A60822; MUID:88293549; PMID:3041969
 A:Accession: B60822
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <AME>
 A:Cross-references: UNIPROT:Q7M068
 C:Genetics:
 A:Gene: CYP2C
 C:Superfamily: cytochrome P450 homology
 C:Keywords: heme

Query Match 26.1%; Score 23; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 2.2e+03;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 VLLRAGFYAVSFL 14
 :|||
 Db 6 VLALTIGFYVYFV 19

RESULT 11

PQ0784

NADH2 dehydrogenase (EC 1.6.99.3) 29K chain - fava bean mitochondrion (fragment)
 N:Alternate names: complex I 29K chain; NADH-ubiquinone reductase 29K chain
 C:Species: mitochondrion Vicia faba (fava bean)
 C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C:Accession: PQ0784
 R:Letierme, S.; Boutry, M.
 Plant Physiol. 102, 435-443, 1993
 A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH dehydrogenase) from Vicia faba
 A:Reference number: PQ0775; MUID:94151437; PMID:8108509
 A:Accession: PQ0784
 A:Molecule type: protein
 A:Residues: 1-10 <LET>
 A:Cross-references: UNIPROT:Q7M2G1
 C:Comment: Complex I mitochondrial NADH-ubiquinone reductase, is the first of the 7
 -ranging from 5K to 75K.
 C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone b
 C:Genetics:
 A:Genome: mitochondrion
 C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 25.0%; Score 22; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLRAG 7
 :|||
 Db 3 LLRSG 8

RESULT 12

D41946
 T-cell receptor gamma chain (1a.4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: D41946
 R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 Mol. Cell. Biol. 11, 5902-5909, 1991
 A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma g
 A:Reference number: A41946; MUID:92049316; PMID:1658619
 A:Accession: D41946
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-11 <WHE>
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 22; DB 2; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.9e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLLRAGF 8
 :|||
 Db 4 VLLRSGF 11

RESULT 13

B4995
 alkaline monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - flashlight fish symbiont
 C:Species: flashlight fish symbiont bacterium
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
 C:Accession: B4995
 R:Haygood, M.G.
 Arch. Microbiol. 154, 496-503, 1990
 A:Title: Relationship of the luminous bacterial symbiont of the Caribbean flashlight fi
 genes.
 A:Reference number: A44995; MUID:91076680; PMID:2256783
 A:Accession: B4995
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-18 <HAY>
 A:Cross-references: GB:M36597; NID:92133345; PIDN:AAA91214.1; PID:gl204253
 C:Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 25.0%; Score 22; DB 2; Length 18;

Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 4 LRAGFYAVSPLS 15
Db 1 MKFGLFFQNFLS 12
::|::|::|::|
Db 1 MKFGLFFQNFLS 12

RESULT 14
PH1360
IG heavy chain DJ region (clone C178-122) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1360
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1360
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 22; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 3.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLLLRAG 7
Db 6 LLLLRVG 12
:|::|::|::|

RESULT 15
A39504
octamer-binding protein, Ku-like, 72K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: A39504
R:May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A:Title: Purification and characterization of Ku-2, an octamer-binding protein related to Ku-1
A:Reference number: A39504; MUID:91131605; PMID:1993678
A:Accession: A39504
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <MAY>

Query Match 25.0%; Score 22; DB 2; Length 19;
Best Local Similarity 37.5%; Pred. No. 3.2e+03;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 4 LRAGFYAVSPLS 19
Db 1 VRSGNKAAXLEMDVG 16
:|::|::|::|::|

Search completed: November 16, 2004, 23:31:06
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 23:19:24 ; Search time 188 Seconds
(without alignments)
58.150 Million cell updates/sec

Title: US-10-036-444-5
Perfect score: 88
Sequence: 1 VLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 12441

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match	100%
Maximum Match	100%

Listing first 45 summaries

```
Database :      UniProt_02:*
          1: uniprot_sprot:*
          2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	34	38.6	16	2	P92070	euhadra ber
2	29	33.0	17	2	Q73531	human immu
3	29	33.0	17	2	Q73533	human immu
4	29	33.0	17	2	Q73535	human immu
5	29	33.0	17	2	Q73537	human immu
6	29	33.0	17	2	Q73539	human immu
7	29	33.0	17	2	Q73541	human immu
8	29	33.0	17	2	Q73543	human immu
9	29	33.0	17	2	Q73545	human immu
10	29	33.0	17	2	Q73547	human immu
11	29	33.0	18	2	Q73517	human immu
12	29	33.0	18	2	Q73523	human immu
13	29	33.0	18	2	Q73551	human immu
14	29	33.0	18	2	Q73553	human immu
15	29	33.0	18	2	Q73555	human immu
16	29	33.0	18	2	Q73559	human immu
17	29	33.0	18	2	Q73561	human immu
18	29	33.0	18	2	Q73563	human immu
19	29	33.0	18	2	Q73565	human immu
20	29	33.0	18	2	Q73567	human immu
21	29	33.0	18	2	Q73569	human immu
22	29	33.0	18	2	Q73571	human immu
23	29	33.0	18	2	Q73581	human immu
24	29	33.0	18	2	Q73585	human immu
25	29	33.0	18	2	Q73589	human immu
26	29	33.0	18	2	Q73591	human immu
27	29	33.0	18	2	Q73593	human immu
28	29	33.0	18	2	Q73597	human immu
29	29	33.0	18	2	Q73599	human immu
30	29	33.0	18	2	Q73611	human immu
31	29	33.0	18	2	Q73617	human immu

ALIGNMENTS

RESULT 1

```

P92070      PRELIMINARY;      PRT;      16 AA.
ID   P92070      AC
AC   P92070;      DT
DT   01-MAY-1997 (TREMblrel. 03, Created)
DT   01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT   01-JUN-2003 (T-EMBlrel. 24, Last annotation update)
DE   NADH dehydrogenase subunit 6 (Fragment).
DE   Euhadra herklotsi.
OS   Euhadra herklotsi.
OS   Mitochondrion.
CG   Eukaryota; Metazoa; Mollusca; Gastropoda; Stylommatophora;
OC   Sigambaretha; Helicoidae; Bradybaenidae; Euhadra.
OC   NCBI_TaxID=58912;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hepatopancreas;
RA   Yamazaki N., Ueshima K., Terrett J.A., Yokobori S., Kaifu M.,
RA   Segawa R., Kobayashi T., Nunachi K., Ueda T., Nishikawa K.,
RL   Watanabe K., Thomas R.H.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR   EMBL: Z71694; CAA96364.1; --
DR   PIR: T14224; T14224
DR   GO: GO:0005739; C:mitochondrion; IEA.
FT   NON TER
FT   1
SQ   SEQUENCE      16 AA; 1836 MW; 258908495BFBFCAE CRC64;
      Query Match      38.6%; Score 34; DB 2; Length 16;
      Best Local Similarity 63.6%; Pred. No. 2.6e+02;
      Matches      7; Conservative      1; Mismatches      3; Indels      0; Gaps      0;
QY      8 FYAVSFLSVAV 18
Db      5 FYAVSFLVGV 15

```

RESULT 2

Q73531	PRELIMINARY;	PRT;	17 AA.
ID	Q73531		
AC	Q73531;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)		
DE	Reverse transcriptase (Fragment).		
GN	Name-pol;		
OS	Human immunodeficiency virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11676;		
RN	[1]_TaxID=11676;		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=9624958; PubMed=8624762;		
RX	Cleland A, Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;		
RT	"Evolution of zidovudine resistance-associated genotypes in human		
RT	immunodeficiency virus type 1-infected patients."		

RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).

RN [2]
RP SEQUENCE FROM N.A.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45097; AAB04248.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 1 LLRWGFY 7

RESULT 3

ID Q73533 PRELIMINARY; PRT; 17 AA.
AC Q73533;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45099; AAB04250.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 1 LLRWGFY 7

RESULT 4

ID Q73535 PRELIMINARY; PRT; 17 AA.
AC Q73535;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45099; AAB04250.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 1 LLRWGFY 7

RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45101; AAB04252.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 1 LLRWGFY 7

RESULT 5

ID Q73537 PRELIMINARY; PRT; 17 AA.
AC Q73537;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45103; AAB04254.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 1 LLRWGFY 7

RESULT 6

ID Q73539 PRELIMINARY; PRT; 17 AA.
AC Q73539;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45103; AAB04254.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 1 LLRWGFY 7

```
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45105; AAB04256.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
Db |||||
1 LLRWGIFY 7

RESULT 7
ID Q73541 PRELIMINARY; PRT; 17 AA.
AC Q73541;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45107; AAB04258.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
Db |||||
1 LLRWGIFY 7

RESULT 8
Q73543
ID Q73543 PRELIMINARY; PRT; 17 AA.
```

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AC Q73543;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45109; AAB04260.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
Db |||||
1 LLRWGIFY 7

RESULT 9
Q73545
ID Q73545 PRELIMINARY; PRT; 17 AA.
AC Q73545;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45111; AAB04262.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2143 MW; B311190D583BBFFE CRC64;

Query Match 33.0%; Score 29; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
Db |||||
1 LLRWGIFY 7
```



```

FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2281 MW; B3691E8D583BBFFE CRC64;

Query Match
Best Local Similarity 33.0%; Score 29; DB 2; Length 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 2 LLRWGFY 8

RESULT 14
Q73553 PRELIMINARY; PRT; 18 AA.
AC Q73553;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45119; AAB04270.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2281 MW; B3691E8D583BBFFE CRC64;

Query Match
Best Local Similarity 33.0%; Score 29; DB 2; Length 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 2 LLRWGFY 8

RESULT 15
Q73555 PRELIMINARY; PRT; 18 AA.
AC Q73555;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96242958; PubMed=8624762;
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Leigh Brown A.J.;

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RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45121; AAB04272.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2281 MW; B3691E8D583BBFFE CRC64;

Query Match
Best Local Similarity 33.0%; Score 29; DB 2; Length 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LLRAGFY 9
DB 2 LLRWGFY 8

Search completed: November 16, 2004, 23:34:19
Job time : 188 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 23:08:14 ; Search time 152 Seconds
(without alignments)
44.841 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLLRAGFYAVSFSLVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 662259

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	88	100.0	19	4 AAE02772	Human Nkp
2	88	100.0	19	8 ADQ30925	Human Nkp
3	80	90.9	19	5 AAE32900	Human Nkp
4	34	38.6	19	5 ABG32813	ABG32813 Ligand/re
5	34	38.6	19	8 ADM73944	Adm73944 Ligand/re
6	33	37.5	10	2 AAR73716	Aar73716 Antigen f
7	33	37.5	10	5 ABJ09403	Abj09403 Hepatitis
8	33	37.5	10	8 ADK39530	Adk39530 Hepatitis
9	33	37.5	17	7 ADB99169	Adb99169 Human pro
10	33	37.5	17	8 ADJ32241	Adj32241 Human pro
11	32	36.4	15	2 AAY14402	Aay14402 Peptide C
12	31	35.2	15	5 ABJ09229	Abj09229 Hepatitis
13	31	35.2	15	5 ABJ08937	Abj08937 Hepatitis
14	31	35.2	15	8 ADK39264	Adk39264 Hepatitis
15	31	35.2	19	2 AAR79515	Aar79515 Hepatitis
16	31	35.2	19	2 AAW93299	Aaw93299 C1q pepri
17	30	34.1	9	5 ABJ06705	Abj06705 Hepatitis
18	30	34.1	9	5 ABJ07565	Abj07565 Hepatitis
19	30	34.1	9	5 ABJ08790	Abj08790 Hepatitis
20	30	34.1	9	5 ABJ05879	Abj05879 Hepatitis
21	30	34.1	9	5 ABJ08081	Abj08081 Hepatitis
22	30	34.1	9	5 ABJ09082	Abj09082 Hepatitis
23	30	34.1	9	8 ADK37194	Adk37194 Hepatitis
24	30	34.1	9	8 ADK38749	Adk38749 Hepatitis
25	30	34.1	9	8 ADK37985	Adk37985 Hepatitis

26 30 34.1 9 8 ADK38995 Hepatitis
27 30 34.1 10 2 AAR61502 Peptide f
28 30 34.1 10 2 AAY43872 Immunogen
29 30 34.1 10 5 ABJ06773 Hepatitis
30 30 34.1 10 5 ABJ06169 Hepatitis
31 30 34.1 10 5 ABJ06706 Hepatitis
32 30 34.1 10 5 ABJ09650 Hepatitis
33 30 34.1 10 5 ABJ08163 Hepatitis
34 30 34.1 10 5 ABJ09759 Hepatitis
35 30 34.1 10 5 ABJ07683 Hepatitis
36 30 34.1 10 5 ABJ07704 Hepatitis
37 30 34.1 10 5 ABJ05916 Hepatitis
38 30 34.1 10 5 ABJ09462 Hepatitis
39 30 34.1 10 5 ABJ09899 Hepatitis
40 30 34.1 10 8 ADE97733 Immunogen
41 30 34.1 10 8 ADK37475 Hepatitis
42 30 34.1 10 8 ADK39527 Hepatitis
43 30 34.1 10 8 ADK38053 Hepatitis
44 30 34.1 10 8 ADK37231 Hepatitis
45 30 34.1 10 8 ADK39039 Hepatitis

ALIGNMENTS

RESULT 1

AAE02772
ID AAE02772 standard; peptide; 19 AA.

XX AAE02772;

XX 06-AUG-2001 (first entry)

XX Human Nkp30 receptor transmembrane region sequence.

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
XX melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
XX immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
XX therapy; transmembrane region.

XX Homo sapiens.

XX WO200136630-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.

XX 15-NOV-1999; 99CA-02288307.

XX 15-NOV-1999; 99US-00440514.

XX (INRA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

XX Novel compound, useful for detection and/or quantifying the presence of
XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX Claim 1; Fig 7B; 83pp; English.

XX The invention relates to human Nkp30 receptor and its corresponding cDNA
XX molecule which is involved in natural cytotoxicity mediated by natural
XX killer (NK) cells and antibodies that identify the same. Nkp30 receptor
XX is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
XX expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
XX useful for detecting and/or quantifying the presence of NK cells in a
XX biological sample. The invention also provide kits for detecting and/or
XX quantifying the presence of NK cells, for the selective removal of NK
XX cells from a biological sample, for the positive and selective
XX purification of NK cells from a biological sample and for the in vitro

CC stimulation of NK cell cytotoxicity. The invention further provides a
 CC pharmaceutical composition which is used as a drug for grafting
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft
 CC versus tumour (GvT), and especially graft versus leukaemia (GvL), and for
 CC the prevention, palliation and/or therapy of solid or liquid tumours,
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
 CC microorganism, notably viral infection. Nkp30 antibodies are useful for
 CC identifying Nkp30 natural ligands and allow assessment of the level of
 CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
 CC comparison of this level to the standard physiological one. Hence Nkp30
 CC antibodies are useful in the diagnosis of tumours or of infection. The
 CC present sequence is the transmembrane region of human Nkp30 receptor
 CC
 XX Sequence 19 AA;
 SQ

Query Match 100.0%; Score 88; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19
 Db 1 VLLLRAGFYAVSFSLVAVG 19

RESULT 2
 ADQ30925
 ID ADQ30925 standard; protein; 19 AA.
 XX
 AC ADQ30925;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human Nkp30 transmembrane region.
 XX
 KW Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.
 XX
 OS Homo sapiens.
 XX
 PN WO2004056392-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-EP014716.
 XX
 PR 23-DEC-2002; 2002US-0435344P.
 XX
 PA (INNA-) INNATE PHARMA.
 XX
 PI Romagne F, Andre P;
 XX
 DR WPI; 2004-507595/48.
 XX
 PS Pharmaceutical compositions that stimulate proliferation of natural
 PT killer cells useful for therapy of melanoma, chronic myeloid, and
 PT leukemia, comprise an anti-natural killer cell receptor antibody and
 PT interleukins.
 XX
 PS Claim 3; SEQ ID NO 3; 35pp; English.
 XX
 CC The present sequence is that of the transmembrane region of human Nkp30
 CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by
 CC natural killer (NK) cells, and particularly by mature NK cells. Claimed
 CC pharmaceutical compositions that have a stimulating effect on the
 CC proliferation of NK cells comprise an antibody such as an anti-Nkp30
 CC antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
 CC antibody(ies) and cytokine(s) being administered together or separately
 CC to a subject. The anti-Nkp30 antibody is an isolated antibody or its
 CC antigen-binding fragment which specifically binds to Nkp30 or to a
 CC fragment, including the transmembrane region, of Nkp30. The
 CC pharmaceutical compositions, when used for daily subcutaneous injection,
 CC comprising from 1 mg to 100 mg/kg (body weight) of antibody(ies), and
 CC lower than 1 million units/square meters/day of cytokine(s), are useful

CC for the prevention, palliation and therapy of e.g. melanoma, chronic
 CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
 CC prevention, palliation and therapy (claimed).
 XX Sequence 19 AA;
 SQ

Query Match 100.0%; Score 88; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19
 Db 1 VLLLRAGFYAVSFSLVAVG 19

RESULT 3
 AAEE23900
 ID AAEE23900 standard; peptide; 19 AA.
 XX
 AC AAEE23900;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human Nkp30 receptor peptide.
 XX
 KW KAR-associated protein; KARAP-transduced immune signal; dendritic cell;
 KW antigen presentation; contact sensitivity; multiple sclerosis;
 KW neuroprotective; human; Nkp30 receptor peptide.
 XX
 OS Homo sapiens.
 XX
 PN WO200224940-A2..
 XX
 PD 28-MAR-2002.
 XX
 PF 20-SEP-2001; 2001WO-EP011492.
 XX
 PR 20-SEP-2000; 2000US-0234161P.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Vivier E, Vely F, Tomasello E;
 XX
 DR WPI; 2002-454420/48.
 XX
 PT Identifying KAR-associated protein-transduced immune signal inhibitor,
 PT comprises using cells co-expressing functional KARAP, and engineered
 PT cells and animals that over-express functional KARAP or bear non-
 PT functional KARAP.
 XX
 PS Example 4; Page 45; 89pp; English.
 XX
 CC The present invention relates to a novel method for identifying compounds
 CC capable of inhibiting KAR-associated protein (KARAP)-transduced immune
 CC signals. The method involves using functional and non-functional KARAP,
 CC cells co-expressing functional KARAP, functional receptors transducing
 CC their signal by zeta, gamma or epsilon and engineered cells and animals
 CC over-expressing functional KARAP or bearing non-functional KARAP. The
 CC method is useful for identifying compounds capable of inhibiting KARAP-
 CC transduced immune signals. The KARAP-inhibiting compounds are useful for
 CC impairing the development and maturation of dendritic cells, for
 CC inhibiting the antigen presentation of dendritic cells, by synthesis
 CC inhibition or through inhibition of the migration of dendritic cells, for
 CC making drugs intended for inhibiting dendritic cell development or
 CC maturation, for preparing drugs for the treatment, prevention, palliation
 CC of immune response, where the activation of KAR has to be inhibited and
 CC for the treatment of contact sensitivity or multiple sclerosis. The
 CC present sequence is human Nkp30 receptor peptide which associate with CD3
 CC zeta and FcR gamma. This sequence is used in the exemplification of the
 CC invention
 XX Sequence 19 AA;
 SQ

Query Match 90.9%; Score 80; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLRAGFYAVSFLSVAG 19
|||||
Db 1 LLRAGFYAVSFLSVAG 17

RESULT 4
ABG62813
ID ABG62813 standard; peptide; 19 AA.

XX AC ABG62813;

XX DT 21-AUG-2002 (first entry)

XX DE Ligand/receptor specificity domain #3.

XX KW Ligand/receptor specificity exchanger; antibody; pathogen receptor;
KW bacterial infection; viral infection; yeast infection; cancer;
KW parasitic infection; fungal infection; proliferation; antibacterial;
KW virucide; cytostatic; antifungal; ligand/receptor specificity domain.

XX OS Synthetic.

XX PN WO200224887-A2.

XX PD 28-MAR-2002.

XX PF 19-SEP-2001; 2001WO-IB002327.

XX PR 19-SEP-2000; 2000US-00664025.

XX PA (TRIP-) TRIPEP AB.

XX PI Sallberg M, Flock J;

XX DR WPI; 2002-489707/52.

XX PT Novel ligand/receptor specificity exchanger that redirects antibodies to
PT receptors on pathogen or tumor cell, has specificity domain having ligand
PT for receptor, and antigenic domain having epitope of pathogen or toxin.

XX PS Claim 6; Page 12; 79pp; English.

XX CC The present invention relates to ligand/receptor specificity exchangers
CC comprising at least one specificity domain comprising a ligand for a
CC receptor, and at least one antigenic domain joined to the specificity
CC domain, where the antigenic domain comprises an epitope of a pathogen or
CC toxin. The ligand/receptor specificity exchangers redirect antibodies to
CC receptors present on pathogens. They are useful for preventing and
CC treating human diseases such as bacterial, viral, yeast, parasitic and
CC fungal infections, and cancer. These compositions act by inhibiting
CC proliferation of pathogens, or cancer cells. One of the prophylactic
CC applications of the ligand/receptor specificity exchangers includes
CC coating or crosslinking it to a medical device or implant which include
CC implantable medical devices that tend to serve as foci for infection by a
CC number of bacterial species. ABG62811-ABG62852 represent ligand/receptor
CC specificity domains used in the methods of the present invention

XX SQ Sequence 19 AA;

Query Match 38.6%; Score 34; DB 5; Length 19;
Best Local Similarity 63.6%; Pred. No. 99;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 FYAVSFLSVAV 18
|||||
Db 4 FYALLFLSTCV 14

RESULT 6
AAR73716

ID AAR73716 standard; peptide; 10 AA.

RESULT 5

ADM73944

ID ADM73944 standard; peptide; 19 AA.

XX AC ADM73944;

XX DT 03-JUN-2004 (first entry)

XX DE Ligand/receptor specificity exchanger specificity domain seqid 3.

XX KW cytostatic; antifungal; virucide; antibacterial; antiparasitic;

XX gene therapy; ligand specificity exchanger; specificity domain;

XX KW bacterial receptor; ligand; antigenic domain; cancer; infection; cancer;

XX KW receptor specificity exchanger.

XX OS Synthetic.

XX PN US2003225251-A1.

XX PD 04-DEC-2003.

XX PF 21-FEB-2003; 2003US-00372735.

XX PR 27-APR-1995; 95WO-SE000468.

XX PR 08-DEC-1996; 96US-00737085.

XX PR 08-FEB-1999; 99US-00246258.

XX PR 21-MAR-2000; 2000US-00532106.

XX PR 21-APR-2000; 2000US-00556605.

XX PR 19-SEP-2000; 2000US-00664025.

XX PR 19-SEP-2000; 2000US-00664945.

XX PR 19-APR-2001; 2001US-00839666.

XX PR 20-APR-2001; 2001US-00839447.

XX PR 19-SEP-2001; 2001WO-IB002327.

XX PR 21-MAY-2002; 2002US-00153271.

XX PR 30-AUG-2002; 2002US-00234579.

XX PA (SALL/) SALLBERG M.

XX PI (FLOC/) FLOCK J.

XX PI Sallberg M, Flock J;

XX DR WPI; 2004-022083/02.

XX PT New ligand specificity exchanger comprising specificity or antigenic
PT domain, useful in preparing a composition for treating e.g., cancer or
PT infections caused by virus, bacteria, parasite, fungus or yeast.

XX PS Disclosure; SEQ ID NO 3; 65pp; English.

XX CC The invention describes a new ligand specificity exchanger comprising a
CC specificity domain comprising a ligand for a bacterial receptor and an
CC antigenic domain joined to the specificity domain and comprising at least
CC 5 and less than 200 consecutive amino acids of a protein from a pathogen
CC or toxin. The ligand specificity exchanger is useful in preparing a
CC composition for treating e.g., cancer or infections caused by virus,
CC bacteria, parasite, fungus or yeast by redirecting existing antibodies to
CC pathogens and cancer cells. This is the amino acid sequence of a
CC ligand/receptor specificity exchanger specificity domain.

XX SQ Sequence 19 AA;

Query Match 38.6%; Score 34; DB 8; Length 19;

Best Local Similarity 63.6%; Pred. No. 99;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 FYAVSFLSVAV 18

|||||

Db 4 FYALLFLSTCV 14

XX AAR73716;
 XX AC
 XX Hepatitis B virus.
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1995 (first entry)
 XX PN
 XX WO200219986-A1.
 XX PD
 XX 14-MAR-2002.
 XX PF
 XX 08-SEP-2000; 2000WO-US024802.
 XX PR
 XX 08-SEP-2000; 2000WO-US024802.
 XX PA
 XX (EPIM-) EPIMMUNE INC.
 XX PA
 XX (SETT/) SETTE A.
 XX PI
 XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 XX PI
 XX Celis B, Kubo RT, Grey HM, Chesnut RW;
 XX DR
 XX WPI; 2002-643192/59.
 XX XX
 XX Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a
 PT HBV peptide epitope.
 PT
 XX Disclosure; Page 188; 228pp; English.
 XX CC
 XX The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention
 XX
 XX Sequence 10 AA;
 QY Query Match 37.5%; Score 33; DB 5; Length 10;
 DB Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 2 LLLRAGFYAV 11
 1 LMLQAGFLV 10
 RESULT 8
 ID ADK39530 standard; peptide; 10 AA.
 XX AC
 XX ADK39530;
 XX DT
 XX 06-MAY-2004 (first entry)
 XX DE
 XX Hepatitis B virus (HBV) epitope #2398.
 XX KW
 XX HBV; cytotoxic T-cell response; immunogenic activity;
 XX KW
 XX human leukocyte antigen; HLA; HBV infection; HBV epitope;
 XX KW
 XX antiinflammatory; hepatotropic; virucide.
 XX OS
 XX Hepatitis B virus.
 XX PN
 XX US6689363-B1.
 XX PD
 XX 10-FEB-2004.
 XX PF
 XX 27-JAN-1999; 99US-00239043.
 XX PR
 XX 29-JAN-1992; 92US-00827682.
 XX PR
 XX 27-APR-1992; 92US-00874491.
 XX PR
 XX 07-AUG-1992; 92US-00926666.
 XX PR
 XX 26-AUG-1992; 92US-00935811.
 XX PR
 XX 05-MAR-1993; 93US-00027146.
 XX PR
 XX 05-MAR-1993; 93US-00027746.
 XX PR
 XX 04-JUN-1993; 93US-00073205.
 XX PR
 XX 06-AUG-1993; 93US-00103396.
 Antigen fragment 32, from HBV (a) has binding affinity for HLA-2.1.
 antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV; HIV1;
 KW plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
 KW melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
 KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
 KW 10mer; anchor; human leukocyte antigen; PUP; 8mer; algorithm prediction;
 KW MBP; CMV; cytomegalovirus; HSV; herpes simplex virus; influenza A; M1.
 XX OS
 XX Hepatitis B virus.
 XX PN
 XX WO9420127-A1.
 XX PD
 XX 15-SEP-1994.
 XX PF
 XX 04-MAR-1994; 94WO-US002353.
 XX PR
 XX 05-MAR-1993; 93US-00027146.
 XX PR
 XX 04-JUN-1993; 93US-00073205.
 XX PR
 XX 29-NOV-1993; 93US-00159184.
 XX PA
 XX (CYTE-) CYTEL CORP.
 XX PI
 XX Grey HM, Sette A, Sidney J, Kast W;
 XX DR
 XX WPI; 1994-302678/37.
 XX XX
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
 PT treatment or prophylaxis of cancer, virus infection or autoimmune
 PT diseases.
 XX
 XX Disclosure; Page 80; 138pp; English.
 XX CC
 XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from the HBV ENV(a)
 CC molecule has a binding value of 0.6300. The peptides of the invention can
 CC induce cytotoxic T lymphocytes which can react with target cells. They
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 10 AA;
 QY Query Match 37.5%; Score 33; DB 2; Length 10;
 DB Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 2 LLLRAGFYAV 11
 1 LMLQAGFLV 10
 RESULT 7
 ID ABJ09403 standard; peptide; 10 AA.
 XX AC
 XX ABJ09403;
 XX DT
 XX 14-NOV-2002 (first entry)
 XX DE
 XX Hepatitis B virus analogue #15.
 XX KW
 XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

virucide; hepatotropic; antiinflammatory.
 XX Hepatitis B virus.
 XX WO200219986-A1.
 XX 14-MAR-2002.
 XX 08-SEP-2000; 2000WO-US024802.
 XX 08-SEP-2000; 2000WO-US024802.
 XX (EPIM-) EPIMMUNE INC.
 XX (SETT/) SETTE A.
 XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 XX Celis B, Kubo RT, Grey HM, Chesnut RW;
 WPI; 2002-643192/59.
 Vaccine composition for treating or preventing hepatitis B virus (HBV) infection, and/or for stimulating an immune response to HBV, comprises a
 HBV peptide epitope.
 Disclosure; Page 188; 228pp; English.
 The present invention relates to a composition comprising at least one
 hepatitis B virus epitope. This can be used in the production of a
 vaccine for use in preventing or treating hepatitis B virus infection.
 The present sequence is a peptide described in the exemplification of the
 invention
 Sequence 10 AA;
 Query Match 37.5%; Score 33; DB 5; Length 10;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 2 LLLRAGFYAV 11
 1 LMLQAGFLV 10
 RESULT 8
 ID ADK39530 standard; peptide; 10 AA.
 XX AC
 XX ADK39530;
 XX DT
 XX 06-MAY-2004 (first entry)
 XX DE
 XX Hepatitis B virus (HBV) epitope #2398.
 XX KW
 XX HBV; cytotoxic T-cell response; immunogenic activity;
 XX KW
 XX human leukocyte antigen; HLA; HBV infection; HBV epitope;
 XX KW
 XX antiinflammatory; hepatotropic; virucide.
 XX OS
 XX Hepatitis B virus.
 XX PN
 XX US6689363-B1.
 XX PD
 XX 10-FEB-2004.
 XX PF
 XX 27-JAN-1999; 99US-00239043.
 XX PR
 XX 29-JAN-1992; 92US-00827682.
 XX PR
 XX 27-APR-1992; 92US-00874491.
 XX PR
 XX 07-AUG-1992; 92US-00926666.
 XX PR
 XX 26-AUG-1992; 92US-00935811.
 XX PR
 XX 05-MAR-1993; 93US-00027146.
 XX PR
 XX 05-MAR-1993; 93US-00027746.
 XX PR
 XX 04-JUN-1993; 93US-00073205.
 XX PR
 XX 06-AUG-1993; 93US-00103396.

PT New isolated polypeptide designated as prostate-specific membrane
PT antigen, useful for diagnosing, preventing or treating prostate cancer in
PT a patient.
XX
XX Disclosure; SEQ ID NO 38; 170pp; English.
XX
XX The invention relates to an isolated polypeptide designated prostate-
CC specific membrane (PSM) antigen. The PSM antigen is useful in diagnosing,
CC preventing or treating prostate cancer in a patient or in isolating
CC homologous gene or genes in different mammals. The present sequence
CC represents the amino acid sequence of the human prostate specific
CC membrane antigen associated peptide.
XX
XX Sequence 17 AA;
SQ

Query Match 37.5%; Score 33; DB 7; Length 17;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0

QY 2 LLLRAGFYAVSFL 14
|:|:|:|:|:
Db 4 LVLGGFFLLGFL 16

RESULT 10
ADJ93241
ID ADJ93241 standard; peptide; 17 AA.
XX
XX AC ADJ93241;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human prostate-specific membrane antigen-related peptide SeqID38.
XX
XX DE alternatively spliced; prostate-specific membrane; PSM; antigen;
KW prostate cell; cytotoxic chemotherapeutic agent; prostate cancer imaging;
KW human.
XX
XX OS Homo sapiens.
OS
XX
XX US2004001846-A1.
XX
XX PD 01-JAN-2004.
XX
XX PP 21-MAY-2003; 2003US-00443694.
XX
XX PR 24-FEB-1995; 95US-00394152.
XX PR 23-FEB-1996; 96WO-US002424.
XX PR 29-AUG-1996; 96US-00705477.
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Israeli RS, Heston WDW, Fair WR, Ouerfelli O, Pinto J;
PI WPI; 2004-061649/06.
XX
XX Isolated polypeptide having biological activity of alternatively spliced
PT prostate-specific membrane antigen, useful for identifying ligands useful
PT in imaging prostate cancer in human patient's.
XX
XX Disclosure; SEQ ID NO 38; 174pp; English.
XX
XX This invention relates to a novel isolated polypeptide having the
CC biological activity of an alternatively spliced prostate-specific
CC membrane (PSM) antigen. The invention is useful for making prostate cells
CC susceptible to a cytotoxic chemotherapeutic agent which involves
CC contacting prostate cells with the polypeptide of the invention in an
CC amount effective to render the prostate cells susceptible to the agent.
CC In addition, the invention is useful for identifying ligands that bind
CC PSM which are useful for imaging prostate cancer in human patients. The
CC present sequence is that of a peptide which is related to the invention.
XX
XX Sequence 17 AA;
SQ

Query Match 37.5%; Score 33; DB 8; Length 17;
 Best Local Similarity 46.2%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLRAGFYAVSFL 14
 | : | | : | : |
 Db 4 LVLGGFFLLGL 16

RESULT 11

AA14402
 ID AAY14402 standard; peptide; 15 AA.

XX AC AAY14402;

XX DT 17-AUG-1999 (first entry)

XX DE Peptide CDR-H3 derived from anti-HCV Ser/Thr protease MAb 8D4.

XX KW Complementarity determining region; CDR; monoclonal antibody; Mab;

XX KW hepatitis C virus; HCV; protease; binding site.

XX OS Synthetic.

XX PN JP11127861-A.

XX PD 18-MAY-1999.

XX PF 29-OCT-1997; 97JP-00297451.

XX PR 29-OCT-1997; 97JP-00297451.

XX PA (NIHA) JAPAN ENERGY CORP.

XX DR WPI; 1999-350322/30.

XX PT Neutralized antibody partial peptide derived from hepatitis C virus -
 useful for inhibiting Hepatitis C Virus (HCV) serine protease activity.

XX PS Example 1; Page 13; 32pp; Japanese.

XX CC This sequence represents a peptide derived for the sequence of the heavy
 chain variable region complementarity determining region (CDR)-3 of the
 anti-hepatitis C virus (HCV) Ser/Thr protease monoclonal antibody (Mab)
 8D4 protein. The invention relates to the use of partial peptides
 CC (AA14348-Y14353) from the Mab 8D4 for inhibiting HCV serine protease
 CC activity

XX SQ Sequence 15 AA;

Query Match 36.4%; Score 32; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RAGFYAVSF 13

Db 3 RGGFYAMDY 11

RESULT 12

ABJ09229
 ID ABJ09229 standard; peptide; 15 AA.

XX AC ABJ09229;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #3447.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

XX KW virucide; hepatotropic; antiinflammatory.

XX

OS Hepatitis B virus.

XX PN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US024802.

XX PR 08-SEP-2000; 2000WO-US024802.

XX PA (EPIM-) EPIMMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;

XX DR WPI; 2002-643192/69.

XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises a
 PT HBV Peptide epitope.

XX PS Disclosure; Page 182; 228pp; English.

XX CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention

XX SQ Sequence 15 AA;

Query Match 35.2%; Score 31; DB 5; Length 15;

Best Local Similarity 41.7%; Pred. No. 2.4e+02;

Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLLRAGFYAVS 12

Db 4 LLVLQAGFFLLT 15

RESULT 13

ABJ08937
 ID ABJ08937 standard; peptide; 15 AA.

XX AC ABJ08937;

XX DT 14-NOV-2002 (first entry)

XX DE Hepatitis B virus epitope #3155.

XX KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.

XX OS Hepatitis B virus.

XX PN WO200219986-A1.

XX PD 14-MAR-2002.

XX PF 08-SEP-2000; 2000WO-US024802.

XX PR 08-SEP-2000; 2000WO-US024802.

XX PA (EPIM-) EPIMMUNE INC.

XX PA (SETT/) SETTE A.

XX PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;

XX DR WPI; 2002-643192/69.

XX PT Vaccine composition for treating or preventing hepatitis B virus (HBV)

Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVS 12

Db 7 LLVLQAGFFLLT 18

Search completed: November 16, 2004, 23:21:58
Job time : 154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 23:22:05 ; Search time 136 Seconds

(without alignments)
49.431 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 267118

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCRUS_PUBCOMB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pap.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pap.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	19	13	US-10-036-444-5
2	34	38.6	19	14	Sequence 5, Appli
3	34	38.6	19	15	Sequence 3, Appli
4	33	37.5	17	15	Sequence 3, Appli
5	33	37.5	17	17	Sequence 38, Appl
6	30	34.1	12	17	Sequence 38, Appl
7	30	34.1	14	10	Sequence 3, Appli
8	30	34.1	14	14	Sequence 3064, Ap
9	29	33.0	16	9	Sequence 3178, Ap
10	28	31.8	10	10	Sequence 82, Appl
11	28	31.8	16	14	Sequence 3178, Ap
12	28	31.8	19	9	Sequence 121, App
13	28	31.8	19	11	Sequence 8, Appli

14	28	31.8	19	14	US-10-219-834-172	Sequence 128, App
15	27	30.7	10	8	US-08-344-824-172	Sequence 172, App
16	27	30.7	11	14	US-10-410-894-24	Sequence 24, Appl
17	27	30.7	12	14	US-10-168-119-3	Sequence 3, Appli
18	27	30.7	16	14	US-10-267-251-12	Sequence 12, Appl
19	27	30.7	19	10	US-09-759-130B-291	Sequence 291, App
20	27	30.7	19	14	US-10-189-123-21	Sequence 21, Appl
21	27	30.7	19	14	US-10-188-495-21	Sequence 21, Appl
22	27	30.7	19	16	US-10-741-790-291	Sequence 291, App
23	26.5	30.1	17	10	US-09-903-190-18	Sequence 18, Appl
24	26.5	30.1	17	14	US-10-319-763-18	Sequence 18, Appl
25	26	29.5	10	14	US-10-216-122-58	Sequence 58, Appl
26	26	29.5	15	9	US-09-286-240-17	Sequence 17, Appl
27	26	29.5	15	10	US-09-912-414-38	Sequence 38, Appl
28	26	29.5	17	9	US-09-864-761-48339	Sequence 48339, A
29	26	29.5	18	14	US-10-084-813-55	Sequence 55, Appl
30	26	29.5	18	14	US-10-084-813-56	Sequence 56, Appl
31	26	29.5	18	14	US-10-084-813-126	Sequence 126, App
32	26	29.5	18	14	US-10-084-813-127	Sequence 127, App
33	26	29.5	18	14	US-10-437-038-14	Sequence 14, Appl
34	26	29.5	18	15	US-10-359-091-14	Sequence 14, Appl
35	26	29.5	19	14	US-10-280-066-54	Sequence 54, Appl
36	25	28.4	7	9	US-09-192-854-133	Sequence 133, App
37	25	28.4	7	9	US-09-968-561A-237	Sequence 237, App
38	25	28.4	7	9	US-09-909-460-83	Sequence 83, Appl
39	25	28.4	7	10	US-09-968-744A-237	Sequence 237, App
40	25	28.4	7	11	US-09-968-561A-237	Sequence 83, Appl
41	25	28.4	7	11	US-09-872-836-83	Sequence 12, Appl
42	25	28.4	9	10	US-09-863-054-12	Sequence 41, Appl
43	25	28.4	9	14	US-10-128-711-41	Sequence 179, App
44	25	28.4	9	14	US-10-371-525-179	Sequence 179, App
45	25	28.4	9	14	US-10-371-069-179	Sequence 179, App

ALIGNMENTS

RESULT 1
US-10-036-444-5
; Sequence 5, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-FR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-5

Query Match 100.0%; Score 88; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFLSVAVG 19

Db 1 VLLLRAGFYAVSFLSVAVG 19

RESULT 2

US-10-372-735-3

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; Sequence 3, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Saliberg, Matti
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUCPE1
; CURRENT APPLICATION NUMBER: US/10/372,735
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/664,025
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/IB01/02327
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 10/153,271
; PRIOR FILING DATE: 2002-05-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptides
US-10-372-735-3
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Query Match 38.6%; Score 34; DB 14; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 8 FYAVSFSLVAV 18
|||: |||: |
Db 4 FYALLFLSTCV 14
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RESULT 3
US-10-608-541-3
; Sequence 3, Application US/10608541
; Publication No. US20040019189A1
; GENERAL INFORMATION:
; APPLICANT: Matti Saliberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPEP.007CE3C1
; CURRENT APPLICATION NUMBER: US/10/608,541
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE 95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: SE 9401460
; PRIOR FILING DATE: 1994-04-28
; NUMBER OF SEQ ID NOS: 105
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Specificity domain peptide
US-10-608-541-3
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Query Match 38.6%; Score 34; DB 15; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY 8 FYAVSFSLVAV 18
|||: |||: |
Db 4 FYALLFLSTCV 14
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RESULT 4
US-10-443-694-38
; Sequence 38, Application US/10443694
; Publication No. US20040001846A1
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; APPLICANT: Overfelli, Ouathek
; APPLICANT: Pinto, John
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1769/41426-GB
; CURRENT APPLICATION NUMBER: US/10/443,694
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 08/705,477
; PRIOR FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-694-38
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Query Match 37.5%; Score 33; DB 15; Length 17;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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QY 2 LLLRAGFYAVSFL 14
|||: |||: |
Db 4 LVLGGFFLLGFL 16
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RESULT 5
US-10-614-625-38
; Sequence 38, Application US/10614625
; Publication No. US20040198657A1
; GENERAL INFORMATION:
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Overfelli, Ouathek
; APPLICANT: Pinto, John
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1769/41426-GB
; CURRENT APPLICATION NUMBER: US/10/614,625
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 10/433,694
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 08/705,477
; PRIOR FILING DATE: 1996-08-29
; PRIOR APPLICATION NUMBER: PCT/US96/02424
; PRIOR FILING DATE: 1996-02-23
; PRIOR APPLICATION NUMBER: US 08/466,381
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/470,735
; PRIOR FILING DATE: 1995-06-06
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; PRIOR APPLICATION NUMBER: US 08/394,152
; PRIOR FILING DATE: 1995-02-24
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-614-625-38

Query Match 37.5%; Score 33; DB 17; Length 17;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 LLLRAGFYAVSFL 14
|:|:|:|:
Db 4 LVLQAGPFLLT 16

RESULT 6

US-10-433-492-3
; Sequence 3, Application US/10433492
; Publication No. US20040202676A1
; GENERAL INFORMATION:
; APPLICANT: CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
; TITLE OF INVENTION: METHOD FOR OBTAINING ANTIGENIC AGGREGATES AND THEIR USE IN FORMUL
; FILE REFERENCE: AGREG
; CURRENT APPLICATION NUMBER: US/10/433,492
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 2000-0279
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
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; NAME/KEY: PEPTIDE
; LOCATION: (1)...(12)
US-10-433-492-3

Query Match 34.1%; Score 30; DB 17; Length 12;
Best Local Similarity 45.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLLRAGFYAVS 12
|:|:|:|:
Db 1 LVLQAGPFLLT 11

RESULT 7

US-09-880-748-3064
; Sequence 3064, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3064
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3064

Query Match 34.1%; Score 30; DB 10; Length 14;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGFYAVSF 13
|:|:|:|:
Db 5 SGYYFVSF 12

RESULT 8

US-10-293-418-3064
; Sequence 3064, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3064
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3064

Query Match 34.1%; Score 30; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGFYAVSF 13
|:|:|:|:
Db 5 SGYYFVSF 12

RESULT 9

US-09-828-708-82
; Sequence 82, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; TITLE OF INVENTION: Autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82

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; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-82

Query Match      33.0%; Score 29; DB 9; Length 16;
Best Local Similarity 75.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SFLSVAVG 19
Db 2 SFLSASVG 9

RESULT 10
US-09-572-404B-3178
; Sequence 3178, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Protpatent version 1.0
; SEQ ID NO 3178
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Sequence located in GART OR PRGS at 420-429 and may interact with
; OTHER INFORMATION: Sequence 3177 in this patent.
US-09-572-404B-3178

Query Match      31.8%; Score 28; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GFYAVSFL 14
Db 3 GFRAIAFL 10

RESULT 11
US-10-014-340-121
; Sequence 121, Application US/10014340
; Publication No. US2003006411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: Diagnosis and Treatment of Alzheimer's Disease
; CURRENT APPLICATION NUMBER: US/10/014.340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 121
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-121

Query Match      31.8%; Score 28; DB 14; Length 16;
Best Local Similarity 63.6%; Pred. No. 9.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 YAVSFLSVAVG 19
Db 2 YAVSTVPVADG 12

RESULT 12

```

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US-09-832-312-8
; Sequence 8, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832.312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-8

Query Match      31.8%; Score 28; DB 9; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLLLRAGFYA 10
Db 10 ILIILAGFLA 19

RESULT 13
US-09-829-495-8
; Sequence 8, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829.495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-8

Query Match      31.8%; Score 28; DB 11; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLLLRAGFYA 10
Db 10 ILIILAGFLA 19

```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 172:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-344-824-172

Query Match      30.7%; S
Best Local Similarity 62.5%; P
Matches 5; Conservative 3;

Qy      1 VLLVQAGF 8
Db      3 LLLVQAGF 10

Search completed: November 16, 2004
Job time : 137 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 23:16:39 ; Search time 38 Seconds
(without alignments)
33.159 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 179518

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	38.6	19	4	US-09-664-945-3
2	33	37.5	10	4	US-09-239-043D-2398
3	33	37.5	17	1	US-08-325-553-38
4	33	37.5	17	2	US-08-394-152A-38
5	33	37.5	17	4	US-08-705-477E-38
6	31	35.2	15	4	US-09-239-043D-2132
7	30	34.1	9	4	US-09-239-043D-62
8	30	34.1	9	4	US-09-239-043D-853
9	30	34.1	9	4	US-09-239-043D-1617
10	30	34.1	9	4	US-09-239-043D-1863
11	30	34.1	10	4	US-09-239-043D-99
12	30	34.1	10	4	US-09-239-043D-343
13	30	34.1	10	4	US-09-239-043D-854
14	30	34.1	10	4	US-09-239-043D-921
15	30	34.1	10	4	US-09-239-043D-1664
16	30	34.1	10	4	US-09-239-043D-1907
17	30	34.1	10	4	US-09-239-043D-2395
18	30	34.1	11	4	US-09-239-043D-344
19	30	34.1	11	4	US-09-239-043D-359
20	30	34.1	11	4	US-09-239-043D-413
21	30	34.1	11	4	US-09-239-043D-855
22	30	34.1	11	4	US-09-239-043D-922
23	30	34.1	11	4	US-09-239-043D-1090
24	30	34.1	11	4	US-09-239-043D-1559
25	30	34.1	12	2	US-08-637-759B-416
26	30	34.1	12	3	US-08-871-355A-416
27	30	34.1	12	3	US-09-201-945-416

28 30 34.1 15 4 US-09-239-043D-2182 Sequence 2182, Ap
29 30 34.1 17 3 US-09-025-769B-257 Sequence 257, App
30 30 34.1 17 4 US-09-490-070A-257 Sequence 257, App
31 30 34.1 17 4 US-09-490-153-357 Sequence 257, App
32 30 34.1 18 3 US-08-788-231A-11 Sequence 11, Appl
33 30 34.1 18 4 US-09-496-239A-12 Sequence 12, Appl
34 30 34.1 19 3 US-08-788-231A-3 Sequence 3, Appl
35 30 34.1 19 4 US-09-496-239A-3 Sequence 3, Appl
36 29 33.0 8 4 US-09-239-043D-82 Sequence 82, Appl
37 29 33.0 8 4 US-09-239-043D-871 Sequence 871, App
38 29 33.0 8 4 US-09-239-043D-1633 Sequence 1633, Ap
39 29 33.0 9 4 US-09-239-043D-357 Sequence 357, App
40 29 33.0 9 4 US-09-239-043D-872 Sequence 872, App
41 29 33.0 10 4 US-09-239-043D-358 Sequence 358, App
42 29 33.0 10 4 US-09-239-043D-873 Sequence 873, App
43 28 31.8 9 4 US-09-239-043D-2465 Sequence 2465, Ap
44 28 31.8 19 3 US-09-345-468-8 Sequence 8, Appl
45 28 31.8 19 3 US-09-414-453A-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-664-945-3
; Sequence 3, Application US/09664945
; Patent No. 6660842
; GENERAL INFORMATION:
; APPLICANT: Matti Sellberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPEP.007CF3
; CURRENT APPLICATION NUMBER: US/09/664,945
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: SE 9401460
; PRIOR FILING DATE: 1994-04-28
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Specificity domain peptide
US-09-664-945-3

Query Match 38.6%; Score 34; DB 4; Length 19;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 FYAVSFLSVAV 18
Db 4 FYALLFLSTCV 14

RESULT 2
US-09-239-043D-2398
; Sequence 2398, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.

```

; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2398
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV analog peptide VM2.LV
US-09-239-043D-2398

Query Match 37.5%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LLLRAGFYAV 11
|:|:|:|:|
Db 1 LMLQAGFELV 10

RESULT 3
US-08-325-553-38
; Sequence 38, Application US/08325553
; Patent No. 5538866
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,553
; FILING DATE:

; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2398
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV analog peptide VM2.LV
US-09-239-043D-2398

Query Match 37.5%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LLLRAGFYAV 11
|:|:|:|:|
Db 1 LMLQAGFELV 10

RESULT 3
US-08-325-553-38
; Sequence 38, Application US/08325553
; Patent No. 5538866
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,553
; FILING DATE:

; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2398
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV analog peptide VM2.LV
US-09-239-043D-2398

Query Match 37.5%; Score 33; DB 1; Length 17;
Best Local Similarity 46.2%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LLLRAGFYAVSFL 14
|:|:|:|:|:|
Db 4 LVLGGFLLGFL 16

RESULT 4
US-08-394-152A-38
; Sequence 38, Application US/08394152A
; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM 330 466 DX2
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,152A
; FILING DATE: 24-FEB-95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41426-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Carcinoma
; IMMEDIATE SOURCE:
; CLONE: Prostate Specific Membrane Antigen
; US-08-394-152A-38

Query Match          37.5%; Score 33; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LLLRAGFYAVSFL 14
   |::||::|
Db 4 LVLGGFFLLGFL 16

RESULT 5
US-08-705-477E-38
; Sequence 38, Application US/08705477E
; Patent No. 6569432
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; APPLICANT: Overfelli, Ouathek
; APPLICANT: Pinto, John
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1769/41426-G
; CURRENT APPLICATION NUMBER: US/08/705,477E
; CURRENT FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-705-477E-38

Query Match          37.5%; Score 33; DB 4; Length 17;
Best Local Similarity 46.2%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LLLRAGFYAVSFL 14
   |::||::|
Db 4 LVLGGFFLLGFL 16

RESULT 6
US-08-239-043D-2132
; Sequence 2132, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D

Query Match          35.2%; Score 31; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 63;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVS 12
   |::||::|
Db 4 LLLVQAGFFLLT 15

RESULT 7
US-09-239-043D-62
; Sequence 62, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D

Query Match          35.2%; Score 31; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 63;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVS 12
   |::||::|
Db 4 LLLVQAGFFLLT 15

US-09-239-043D-2132
; ORGANISM: Orthohepadnaviridae hepatitis B virus
; QUERY MATCH          35.2%; Score 31; DB 4; Length 15;
; BEST LOCAL SIMILARITY 41.7%; Pred. No. 63;
; MATCHES 5; CONSERVATIVE 6; MISMATCHES 1; INDELS 0; GAPS 0;

; REMAINING PRIOR APPLICATION DATA REMOVED - SEE FILE WRAPPER OR PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2132
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; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-62

Query Match      34.1%; Score 30; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3.8e+05;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLLLRAGFY 9
Db      1 LLVLQAGFF 9
      :|:|:|:|:|:

RESULT 8
US-09-239-043D-853
; Sequence 853, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 08/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 853
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-853
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Query Match      34.1%; Score 30; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3.8e+05;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLLLRAGFY 9
Db      1 LLVLQAGFF 9
      :|:|:|:|:|:

RESULT 9
US-09-239-043D-1617
; Sequence 1617, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 08/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1617
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1617

Query Match      34.1%; Score 30; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3.8e+05;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLLLRAGFY 9
Db      1 LLVLQAGFF 9
      :|:|:|:|:|:

RESULT 10
US-09-239-043D-1863
; Sequence 1863, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
```

```
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1863
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1863

Query Match      34.1%; Score 30; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3.8e+05;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLLLRAGFY 9
        :|:|:|:|:
Db      1 LLLVQAGFF 9

RESULT 11
US-09-239-043D-99
; Sequence 99, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1863
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1863

Query Match      34.1%; Score 30; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3.8e+05;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLLLRAGFY 9
        :|:|:|:|:
Db      1 LLLVQAGFF 9

RESULT 12
US-09-239-043D-343
; Sequence 343, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
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; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-854
Query Match      34.1%; Score 30; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFY 9
   :|:|:|:|:
Db 1 LLVLQAGFF 9

RESULT 13
US-09-239-043D-854
; Sequence 854, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 854
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-854
Query Match      34.1%; Score 30; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFY 9
   :|:|:|:|:
Db 1 LLVLQAGFF 9

RESULT 14
US-09-239-043D-921
; Sequence 921, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 921
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-921
Query Match      34.1%; Score 30; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFY 9
   :|:|:|:|:
Db 2 LLVLQAGFF 10

RESULT 15
US-09-239-043D-1664
; Sequence 1664, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott

```

```

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFY 9
   :|:|:|:|:
Db 1 LLVLQAGFF 9

RESULT 14
US-09-239-043D-921
; Sequence 921, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 921
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-921
Query Match      34.1%; Score 30; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFY 9
   :|:|:|:|:
Db 2 LLVLQAGFF 10

RESULT 15
US-09-239-043D-1664
; Sequence 1664, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 22:58:47 ; Search time 38 Seconds
(without alignments)
83.557 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHGTHCHSSDGRGVPEPCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 7182

Minimum DB seq length: 0

Maximum DB seq length: 33

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	18.1	18	A54195	Na+/K+-exchanging
2	37	18.1	21	S47207	T-cell receptor J-
3	34	16.7	26	S55029	CAP3 protein - ant
4	34	16.7	30	B53088	factor IX/factor X
5	33	16.2	27	I47719	house-dust-mite-re
6	33	16.2	33	A05136	neurotoxin IX - sc
7	32	15.7	26	1 SMNC	metallothionein -
8	31.5	15.4	26	4 I55277	hemoglobin alpha c
9	31	15.2	16	2 PH1351	Ig heavy chain DJ
10	31	15.2	29	1 Q1BP57	gene 1.5 protein -
11	31	15.2	33	2 B29841	big gastrin - Chin
12	30.5	15.0	28	2 I52841	erythrocyte chemok
13	30	14.7	24	2 B44379	omega-conotoxin SV
14	30	14.7	25	1 SMNR	metallothionein -
15	30	14.7	26	2 S50118	activating factor
16	30	14.7	28	2 A25310	alpha-amylose/tryp
17	30	14.7	30	2 A82137	hypothetical prote
18	29.5	14.5	23	2 T44339	hypothetical prote
19	29.5	14.5	29	2 D32533	class II histocomp
20	29	14.2	16	2 A11488	taurocyamine kinas
21	29	14.2	17	2 S57555	T cell receptor V-
22	29	14.2	25	2 A49038	Ig lambda chain V
23	29	14.2	26	2 S06675	apidaecin Ib precu
24	29	14.2	27	2 JS0676	hypothetical 3.1K
25	29	14.2	28	2 B25310	alpha-amylose/tryp
26	29	14.2	30	2 JC1360	hypothetical 3K pr
27	29	14.2	32	2 S36825	UDP-galactose-N-ac
28	28.5	14.0	28	2 S20393	trypsin inhibitor
29	28.5	14.0	30	2 S12965	gamma-crystallin -

30 28.5 14.0 31 2 A61014 defensin NP-4 - ra
31 28.5 14.0 33 2 PQ0416 RNA-directed RNA p
32 28 13.7 11 2 S42587 celf protein - Esc
33 28 13.7 19 2 S67517 Na+/K+-exchanging
34 28 13.7 23 2 A41263 kinase-related tra
35 28 13.7 28 2 A27261 proteinase inhibit
36 28 13.7 29 2 PC4421 multactivase A2 (
37 28 13.7 32 2 S58413 phospholipase A2 (
38 28 13.7 32 2 C82091 hypothetical prote
39 27.5 13.5 24 2 S42776 relaxin - baboon (
40 27.5 13.5 24 2 S42780 relaxin - orangura
41 27.5 13.5 27 1 T2M23 toxin III - snake-
42 27.5 13.5 33 2 A71297 hypothetical prote
43 27 13.2 10 2 PH0925 T-cell receptor be
44 27 13.2 11 1 XASNBA bradykinin-potent
45 27 13.2 13 2 A61210 antibiotic GE2270

ALIGNMENTS

RESULT 1

A54195

Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C:Species: Scualus acanthias (spiny dogfish)

C:Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A54195

R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-A

A:Reference number: A54195; MUID:94297020; PMID:8025109

A:Accession: A54195

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <ESM>

A:Cross-references: UNIPROT:Q9SPR6

A:Experimental source: rectal gland

A>Note: sequence extracted from NCBI backbone (NCBI:149363)

C:Keywords: hydrolase

Query Match

Best Local Similarity 18.1%; Score 37; DB 2; Length 18;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 21 DQPRGVPEPCP 33

DB 1 DGNALTPPTTP 13

RESULT 2

S47207

T-cell receptor J-alpha wNVIII.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999

C:Accession: S47207

R:Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.

submitted to the EMBL Data Library, February 1993

A:Reference number: S40133

A:Accession: S47207

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-21 <PLA>

A:Cross-references: EMBL:X71032; NID:G506610; PIDN:CAA50349.1; PID:G510318

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 18.1%; Score 37; DB 2; Length 21;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 26 VIPEPCP 33

DB 11 LVPEPCP 18

```

RESULT 3
S55029
CAP3 protein - anthracnose fungus (Colletotrichum gloeosporioides)
C:Species: Glomerella cingulata, Colletotrichum gloeosporioides
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S55029
R:Hwang, C.S.; Kolattukudy, P.E.
Mol. Gen. Genet. 247, 282-294, 1995
A:Title: Isolation and characterization of genes expressed uniquely during appressorium
A:Reference number: S55029; MUID:95287848; PMID:7770033
A:Accession: S55029
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-26 <HWA>
A:Cross-references: UNIPROT:Q99334; EMBL:U18756; NID:g619921; PIDN:AAA77679.1; PID:g6199
C:Genetics:
A:Introns: 24/3
C:Superfamily: metallothionein

Query Match 16.7%; Score 34; DB 2; Length 26;
Best Local Similarity 41.2%; Pred. No. 7.1e+02;
Matches 7; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

Qy 7 GKCHCHMGTHCHSSDGP 23
Db 10 GTCHC--GKDCACGCP 24

RESULT 4
B53088
factor IX/factor X-binding anticoagulant protein A chain - jararaca (fragment)
C:Species: Bothrops jararaca (jararaca)
C:Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B53088
R:Sekiya, F.; Atoda, H.; Morita, T.
Biochemistry 32, 6892-6897, 1993
A:Title: Isolation and characterization of an anticoagulant protein homologous to botroc
A:Reference number: A53088; MUID:93326575; PMID:8334120
A:Accession: B53088
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-30 <SEK>
A:Cross-references: UNIPROT:Q9PS05
A:Experimental source: venom
A:Note: sequence extracted from NCBI backbone (NCBIP:135336)

Query Match 16.7%; Score 34; DB 2; Length 30;
Best Local Similarity 30.0%; Pred. No. 8.1e+02;
Matches 6; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 5 YQKCHCHMGTHCHSSDGP 24
Db 9 YEGHCYHFIRKWMNDAER 28

RESULT 5
I47719
house-dust-mite-reactive T-cell receptor beta chain (CD4+ clone DE5, V(D)J junctional re
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: I47719
R:Wedderburn, L.R.; O'Hehir, R.E.; Hewitt, C.R.; Lamb, J.R.; Owen, M.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8214-8218, 1993
A:Title: In vivo clonal dominance and limited T-cell receptor usage in human CD4+ T-cell
A:Reference number: A47719; MUID:93376774; PMID:8367485
A:Accession: I47719
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-27 <WED>
A:Note: sequence extracted from NCBI backbone (NCBIN:137829, NCBIP:137835)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 16.2%; Score 33; DB 2; Length 27;
Best Local Similarity 66.7%; Pred. No. 9.8e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 17 CHSSDGP 25
Db 1 CASSQGP 9

RESULT 6
A05136
neurotoxin IX - scorpion (Buthus occitanus) (fragment)
C:Species: Buthus occitanus tunetanus
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A05136
R:Martin, M.F.; Rochat, H.
Toxicon 22, 279-291, 1984
A:Title: Purification of thirteen toxins active on mice from the venom of the North Afri
A:Reference number: A94316; MUID:84224814; PMID:6729843
A:Accession: A05136
A:Molecule type: protein
A:Residues: 1-33 <MAR>
A:Cross-references: UNIPROT:P04099
C:Superfamily: scorpion neurotoxin
C:Keywords: neurotoxin

Query Match 16.2%; Score 33; DB 2; Length 33;
Best Local Similarity 27.8%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Qy 3 VYQKGC--HCHMGTHCH 18
Db 10 IVFPNCVYHCGLDPPYCN 27

RESULT 7
SMNC
metallothionein - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 31-May-1980 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A24641; A03287
R:Muenger, K.; Germann, U.A.; Lerch, K.
EMBO J. 4, 2665-2668, 1985
A:Title: Isolation and structural organization of the Neurospora crassa copper metalloth
A:Reference number: A24641; MUID:86030247; PMID:2932331
A:Accession: A24641
A:Molecule type: DNA
A:Residues: 1-26 <MUE>
A:Cross-references: UNIPROT:P02807; GB:X03009; NID:g2986; PIDN:CAA26793.1; PID:g2987
R:Lerch, K.
Nature 284, 368-370, 1980
A:Title: Copper metallothionein, a copper-binding protein from Neurospora crassa.
A:Reference number: A03287; MUID:80143244; PMID:6444697
A:Accession: A03287
A:Molecule type: protein
A:Residues: 2-26 <LER>
C:Genetics:
A:Introns: 18/1
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding; metal-thiolate cluster
F:4,6,12,14,18,20,23/Binding site: transition metal ions (Cys) #status experimental

Query Match 15.7%; Score 32; DB 1; Length 26;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 7 GKCHCHMGTHCHSSDG 22
Db 2 GDCGSGASSCNCGSG 17

RESULT 8
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I55277
hemoglobin alpha chain thalassemia mutant Brooklyn - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 31-May-1996 #text_change 20-Apr-2000
C:Accession: I55277
R:Safaya, S.; Rieder, R.F.
J. Biol. Chem. 263, 4328-4332, 1988
A:Title: Dysfunctional alpha-globin gene in hemoglobin H disease in blacks. A dinucleotide
A:Reference number: I55277; MUID:88153756; PMID:2831226
A:Accession: I55277
A:Molecule type: DNA
A:Residues: 1-26 <SAF>
A:CROSS-references: GB:M22814; NID:g183799; PIDN:AAA52631.1; PID:g183801
A:Note: GenBank entry HUMHBADY2 repeats the normal sequence, which was not redetermined.
C:Genetics:
A:Gene: GDB:HB2
A:CROSS-references: GDB:119294; OMIM:141850
A:Map position: 16p13.3-16p13.3

Query Match 15.4%; Score 31.5; DB 4; Length 26;
Best Local Similarity 47.1%; Pred. No. 1.4e+03;
Matches 8; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 18 HSSDGPGRVPEPR-CP 33
DB 9 HHQDLLPALRPEPR-LCP 25

RESULT 9
PH1351
1g heavy chain DJ region (clone C100-109B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1351
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DUH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1351
A:Molecule type: DNA
A:Residues: 1-16 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 15.2%; Score 31; DB 2; Length 16;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 21 DGPGRGVPEPR-CP 33
DB 4 DGPGRGVPEPR-CP 16

RESULT 10
Q1BP57
Gene 1.5 protein - phage T7
C:Species: phage T7
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: I43002; I43004; S42294; A04417
R:Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, September 1982
A:Reference number: A94615
A:Accession: I43002
A:Molecule type: DNA
A:Residues: 1-29 <DUN>
A:CROSS-references: UNIPROT:P03792
R:Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 148, 303-330, 1981
A:Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be
A:Reference number: A92866; MUID:82078034; PMID:7310871
A:Accession: I43004
A:Molecule type: DNA
A:Residues: 1-29 <DU2>
A:CROSS-references: GB:V01127; NID:g15498; PIDN:CAA24338.1; PID:g15510

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R:Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 g
A:Reference number: S42283; MUID:83241725; PMID:6864790
A:Accession: S42294
A:Molecule type: DNA
A:Residues: 1-29 <DUN>
A:CROSS-references: EMBL:V01146; NID:g431187; PIDN:CAA24395.1; PID:g15574
C:Genetics:
A:Gene: 1.5
A:Map position: 19.48-19.69
C:Superfamily: phage T7 gene 1.5 protein

Query Match 15.2%; Score 31; DB 1; Length 29;
Best Local Similarity 38.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 13 MGTHCHSSDGPGRG 25
DB 15 LALHCSDDDDMPDG 27

RESULT 11
B29541
big gastrin - Chinchilla brevicaudata
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 03-Jul-2004
C:Accession: B29541
R:Shinomura, Y.; Eng, J.; Yalow, R.S.
Biochem. Biophys. Res. Commun. 143, 7-14, 1987
A:Title: Chinchilla "big" and "little" gastrins.
A:Reference number: A90130; MUID:87156784; PMID:3827930
A:Accession: B29541
A:Molecule type: protein
A:Residues: 1-33 <SHI>
A:CROSS-references: UNIPROT:P10034
C:Superfamily: gastrin

Query Match 15.2%; Score 31; DB 2; Length 33;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 12 HMGTHCHSSDGP 23
DB 9 HLGTLSSKKQGP 20

RESULT 12
I52627
erythrocyte chemokine receptor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I52627
R:Mallinson, G.; Soo, K.S.; Schall, T.J.; Pisacka, M.; Anstee, D.J.
Br. J. Haematol. 90, 823-829, 1995
A:Title: Mutations in the erythrocyte chemokine receptor (Duffy) gene: the molecular ba
al with the Fy(a-b-) phenotype.
A:Reference number: I52627; MUID:95399278; PMID:7669660
A:Accession: I52627
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <RES>
A:CROSS-references: GB:S79269; NID:g1086935; PIDN:AAB35274.1; PID:g1086936

Query Match 15.0%; Score 30.5; DB 2; Length 28;
Best Local Similarity 38.9%; Pred. No. 2e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 7 GKCHCHMGTHCHSSDGP 24
DB 12 GQCPLQ---HCGARLGR 26

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RESULT 13

B44379
 omega-conotoxin SVIA - cone shell (Conus striatus)
 N:Alternate names: SNX-157
 C:Species: Conus striatus (striated cone)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: B44379
 R:Ramilo, C.A.; Zafaralla, G.C.; Nadaadi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W.F.
 Biochemistry 31, 9919-9926, 1992
 A:Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
 A:Reference number: A44379; MUID:93003172; PMID:1390774
 A:Accession: B44379
 A:Molecule type: protein
 A:Residues: 1-24 <RAM>
 A:Cross-references: UNIPROT:Q9N604; UNIPROT:Q9NCU3; UNIPROT:Q9NCU4; UNIPROT:Q9NCU2; UNIPROT:Q9NCU1
 A:Experimental source: venom
 A:Note: sequence extracted from NCBI backbone (NCBI:P116001); structure confirmed by chemical synthesis
 C:Comment: This omega-conotoxin blocks presynaptic calcium channels.
 C:Superfamily: omega-conotoxin
 C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inhibitor
 F:1-15,8-18,14-23/Disulfide bonds: #status predicted
 F:24/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 14.7%; Score 30; DB 2; Length 24;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 17 CHSSDGRGV 26
 DB 1 CRSSGSPGV 10

RESULT 14

SNMR
 metallothionein - cultivated mushroom
 C:Species: Agaricus bisporus (cultivated mushroom)
 C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
 C:Accession: A03286
 R:Munger, K.; Lerch, K.
 Biochemistry 24, 6751-6756, 1985
 A:Title: Copper metallothionein from the fungus Agaricus bisporus: chemical and spectroscopic properties
 A:Reference number: A03286
 A:Accession: A03286
 A:Molecule type: protein
 A:Residues: 1-25 <MUN>
 A:Cross-references: UNIPROT:P04358
 A:Experimental source: mycelium; strain A-32
 C:Comment: In contrast to the vertebrate metallothioneins, the fungal proteins bind copper with a 1:1 stoichiometry.
 C:Comment: The absorptive, luminescent, and stereoptical properties of the copper WT are similar to those of the metallothionein.
 C:Superfamily: metallothionein
 C:Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 14.7%; Score 30; DB 1; Length 25;
 Best Local Similarity 31.2%; Pred. No. 2.1e+03;
 Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 7 GKCHCHMGTHCHSSDG 22
 DB 1 GDCGCGASSCTCAG 16

RESULT 15

SE0118
 activating factor (clone 11) - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C>Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: SE0118
 R:Estruch, J.J.; Crossland, L.; Goff, S.A.
 Nucleic Acids Res. 22, 3983-3989, 1994
 A:Title: Plant activating sequences: positively charged peptides are functional as trans-acting factors
 A:Reference number: SE0118; MUID:95023159; PMID:7937121
 A:Accession: SE0118
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA
 A:Residues: 1-26 <EST>
 A:Cross-references: UNIPROT:Q40536; GB:L33875; NID:949885; PIDN:ADA53419.1; PID:949886
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match 14.7%; Score 30; DB 2; Length 26;
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 CHMGTHCHSS 20
 DB 15 CSVDYHAHSS 24

Search completed: November 16, 2004, 23:08:07
 Job time : 40 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	39	19.1	27	2	Q9UMA6 homo sapien
2	38	18.6	26	2	Q96Hm8 homo sapien
3	37	18.1	29	1	SODC OLEEU
4	36	17.6	23	1	Q95376 homo sapien
5	35.5	17.4	33	2	Q9AR83 pinus pinas
6	35	17.2	23	2	Q9AWD7 homo sapien
7	34	16.7	26	1	Q95334 collectotric
8	34	16.7	28	1	MT1 COLGL
9	34	16.7	30	2	SCKZ_ORTSC
10	34	16.7	30	2	Q9PB17 orthochirus
11	34	16.7	30	2	Q9PS05 candida alb
12	33.5	16.4	33	1	TKN1 SELHA
13	33	16.2	33	2	Q9WUJ1 mus musculu
14	33	16.2	33	2	Q7PD61 a ensangp00
15	33	16.2	26	2	Q9LJE7 arabidopsis
16	32.5	15.9	33	1	SCX9 BUTOC
17	32.5	15.9	31	2	Q6BHD5
18	32.5	15.9	33	2	Q7JIT2
19	32.5	15.9	33	2	AA514887
20	32	15.7	25	1	MT1 NEUCR
21	32	15.7	26	2	O56482
22	32	15.7	26	2	O56512
23	32	15.7	27	2	Q9Q9B7
24	32	15.7	28	2	Q9UCG8
25	32	15.7	32	2	O42638
26	32	15.7	32	2	O8TGU8
27	32	15.7	32	2	Q6T3W7
28	32	15.7	32	2	AAK04847
29	32	15.7	33	2	Q8WWE0
30	31.5	15.4	25	2	Q7OWF0
31	31.5	15.4	25	2	CAD57203
32	31.5	15.4	25	2	Q9W5703 aeromonas

RC TISSUE=Uterus; PubMed=12477932;
 RX MEDLINE=42388257; Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshnyuk S., Abramson R.D., Mullaly S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC008359; AA08359.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 26 AA; 2905 MW; 73C384117555A1D9 CRC64;
 Query Match 18.6%; Score 38; DB 2; Length 26;
 Best Local Similarity 53.8%; Pred. No. 9.6e+02;
 Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 10 KCHMGTHCHSDG 22
 DB 12 KTHTHTHPSCG 24
 RESULT 3
 SODC_OLEU STANDARD; PRT; 29 AA.
 ID P80740;
 AC
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e
 V) (Fragment).
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea";
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
 CC InterPro: IPR001424; SOD_CU_ZN.
 DR Pfam: PF00080; SOD_Cu; 1.
 DR PROSITE: PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE: PS00332; SOD_CU_ZN_2; PARTIAL.
 KW Allergen; Antioxidant; Copper; Direct protein sequencing;

KW Metal-binding; Oxidoreductase; Zinc.
 FT NON_TER 29
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;
 Query Match 18.1%; Score 37; DB 1; Length 29;
 Best Local Similarity 46.2%; Pred. No. 1.4e+03;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 15 THCHSSDQPRGVI 27
 DB 5 TVLNSSESGPRGIV 17
 RESULT 4
 Q95376 PRELIMINARY; PRT; 23 AA.
 ID Q95376;
 AC Q95376;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE MHC class II antigen HLA-DRB4*0201N (Fragment).
 GN Name=HLA-DRB4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97306279; PubMed=9162096;
 RA Robbins F., Hurley C.K., Tang T., Yao H., Lin Y.S., Wade J.,
 RA Goeken N., Hartzman R.J.;
 RT "Diversity associated with the second expressed HLA-DRB locus in the
 RT human population";
 RL Immunogenetics 46:104-110(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Robbins F.Y.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50061; AAB63532.1; -;
 FT NON_TER 1
 SQ SEQUENCE 23 AA; 2729 MW; AD6B35DC3A259BBF CRC64;
 Query Match 17.6%; Score 36; DB 2; Length 23;
 Best Local Similarity 71.4%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 QGKCHCH 12
 DB 5 QAKCECH 11
 RESULT 5
 Q9AR83 PRELIMINARY; PRT; 33 AA.
 ID Q9AR83;
 AC Q9AR83;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Putative metallothionein-like protein (fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aerial part;
 RA Dubos C., Le Provost G., Salin F., Lalane C., Madur D., Frigerio J.M.,
 RA Plomion C.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ309103; CAC35976.1; -;
 GO; GO:0046872; F:metal ion binding; IEA.

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DR InterPro: IPR000347; Metallthion 15p.
DR ProDom: PD001611; Metallthion_15p; 1;
FT NON_TER 1
SQ SEQUENCE 33 AA; 3610 MW; A89612AE71CD728C CRC64;

Query Match 17.4%; Score 35.5; DB 2; Length 33;
Best Local Similarity 33.3%; Pred. No. 2.5e+03;
Matches 8; Conservative 5; Mismatches 6; Indels 5; Gaps 2;

QY 1 STVYQKCK-----HCHMGT-HCHS 19
Db 10 NTVHLENDCKGPNCGCGTCSCHT 33

RESULT 6
Q8WWD7 PRELIMINARY; PRT; 23 AA.
AC Q8WWD7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017851; AAH17851.1; -;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2300 MW; CBCB6B3DFCAABD6B CRC64;

Query Match 17.2%; Score 35; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 2e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 13 MGTCHSSDGP 23
Db 7 LGTYCGAAGP 17

RESULT 7
MT1_COLGL STANDARD; PRT; 26 AA.
AC Q99334;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Metallothionein-like protein CAP3.
GN Name=CAP3;
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
OS cingulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
CX NCBI_TaxID=5457;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Conidium;
RX MEDLINE=95287848; PubMed=7770033;
RA Hwang C.-S.; Kolatukudy P.E.;
RT "Isolation and characterization of genes expressed uniquely during
RT appressorium formation by Colletotrichum gloeosporioides conidia
RT induced by the host surface wax."
RL Mol. Gen. Genet. 247:282-294 (1995).
CC -!- DEVELOPMENTAL STAGE: Expressed in the conidium only during the
CC process of appressorium formation induced by avocado surface wax.
CC -!- MISCELLANEOUS: The seven cysteines bind six copper (cuprous) ions
CC (By similarity).

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CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 8.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U18756; AAA77679.1; -.
DR EMBL; L22549; AAA74033.1; -.
DR PIR; S55029; S55029.
DR InterPro: IPR003019; Metallthion_
DR Pfam: PF00131; Metallothio; 1.
KW Copper; Metal-binding; Metal-thiolate cluster.
FT METAL 4 4 6
FT METAL 12 12
FT METAL 14 14
FT METAL 18 18
FT METAL 20 20
FT METAL 23 23
SQ SEQUENCE 26 AA; 2519 MW; CID173B2921BDCFC CRC64;

Query Match 16.7%; Score 34; DB 1; Length 26;
Best Local Similarity 41.2%; Pred. No. 3.1e+03;
Matches 7; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 7 GKCHCHMGTHCHSSDGP 23
Db 10 GTCHC--GKDCCTCAGCP 24

RESULT 8
SCK2_ORTSC STANDARD; PRT; 28 AA.
ID SCK2_ORTSC
AC P83244;
DT 28-FEB-2003 (Rel. 41, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toxin Osk2 (Osk-2) (Alpha-KTX 13.2).
OS Orthochirus scrobiculosus (Central Asian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Euthida; Euthoidea; Euthidae; Orthochirus.
OX NCBI_TaxID=6892;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21418774; PubMed=11527374; DOI=10.1006/bbrc.2001.5492;
RA Dudina E.E.; Korolkova Y.V.; Bocharova N.E.; Koshelev S.G.;
RA Egorov T.A.; Huys I.; Tytgat J.; Grishin E.V.;
RT "Osk2, a new selective inhibitor of Kv1.2 potassium channels purified
RT from the venom of the scorpion Orthochirus scrobiculosus."
RL Biochem. Biophys. Res. Commun. 286:841-847 (2001).
CC -!- FUNCTION: Potent and selective inhibitor of Kv1.2 potassium
CC channels. Does not block Kv1.1 and Kv1.3 currents.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=2892.14; METHOD=VALDI; RANGE=1-28;
CC NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
CC GO: GO:0005576; C:extracellular; NAS.
CC GO: GO:0019870; F:potassium channel inhibitor activity; IDA.
CC GO: GO:0019835; P:cytolysis; IDA.
CC GO: GO:0009405; P:pathogenesis; IDA.
CC InterPro: IPR001947; Scorpion toxins.
CC PROSITE: PS01138; SCORP_SHORT_TOXIN; FALSE NEG.
KW Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor; Toxin.
FT DISULFID 2 19
FT DISULFID 6 24
FT (By similarity).

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FT DISULFID 10 26 By similarity
 FT SITE 17 24 Interaction with Ca(2+)-activated K(+) channels (potential).
 SQ SEQUENCE 28 AA; 2901 MW; A9BD332061F99E5 CRC64;

Query Match 16.7%; Score 34; DB 1; Length 28;
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GKCHCH 12
 Db 22 GSCHCY 27

RESULT 9
 Q9P817 PRELIMINARY; PRT; 30 AA.
 AC Q9P817
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21155066; PubMed=11231566;
 RA De Backer M.D., Nelissen B., Logghe M., Viaene J., Loonen I.,
 RA Vandoninck S., de Hoogt R., Dewaele S., Simons F.A., Verhasselt P.,
 RA Vanhoof G., Contreras R., Luyten W.H.;
 RT "An antisense-based functional genomics approach for identification of
 RT genes critical for growth of *Candida albicans*.";
 RL Nat. Biotechnol. 19:212-213(2001).
 DR EMBL; AJ390525; CAB7661.1; -
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 30
 SQ SEQUENCE 30 AA; 3572 MW; 324ALDB3D1578E64 CRC64;

Query Match 16.7%; Score 34; DB 2; Length 30;
 Best Local Similarity 36.4%; Pred. No. 3.5e+03;
 Matches 8; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

Qy 10 HCMGTHCHSSDPRG--VIVE 29
 Db 8 HVLVSHKHQDSNKGKVIQE 29

RESULT 10
 Q9PS05 PRELIMINARY; PRT; 30 AA.
 AC Q9PS05
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Factor IX-binding protein A chain (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93326575; PubMed=8334120;
 RA Sekiya F., Atoda H., Morita T.;
 RT "Isolation and characterization of an anticoagulant protein homologous
 RT to botrocetin from the venom of *Bothrops jararaca*.";
 RL Biochemistry 32:6892-6897(1993).
 DR PIR; B53088; B53088.
 DR HSP; P23807; I034.
 SQ SEQUENCE 30 AA; 3709 MW; DD49A218EDDBA9D2 CRC64;

Query Match 16.7%; Score 34; DB 2; Length 30;
 Best Local Similarity 30.0%; Pred. No. 3.5e+03;
 Matches 6; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 5 YQKCHCHMGTHCHSSDGR 24
 Db 9 YEGHCYKHFIKWNNEDAER 28

RESULT 11
 TXN1 SELHA STANDARD; PRT; 33 AA.
 AC P83551;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Hainantoxin-I (HnTx-I).
 OS Selenocosmia hainana (Chinese bird spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Ornithoconus.
 OX NCBI_TaxID=209901;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX PubMed=12727268;
 RA Xiao Y.-C., Liang S.-P.;
 RT "Purification and characterization of Hainantoxin-V, a tetrodotoxin-
 RT sensitive sodium channel inhibitor from the venom of the spider
 RT *Selenocosmia hainana*.";
 RL Toxicon 41:643-650(2003).
 RN [2]
 RP REVISIONS TO 30-32, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, MASS SPECTROMETRY, DISULFIDE BONDS, AMIDATION, IC(50),
 RP AND STRUCTURE BY NMR.
 RC TISSUE=Venom;
 RX PubMed=14675784;
 RA Li D.-L., Xiao Y.-C., Hu W.-J., Xie J.-Y., Bosmans F., Tytgat J.,
 RA Liang S.-P.;
 RT "Function and solution structure of hainantoxin-I, a novel insect
 RT sodium channel inhibitor from the Chinese bird spider *Selenocosmia*
 RT *hainana*.";
 RL FEBS Lett. 555:616-622(2003).
 CC -!- FUNCTION: Is a depressant toxin. Binds and blocks insect sodium
 CC channels without altering the activation or inactivation kinetics.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=3608.02; METHOD=MALDI; RANGE=1-33;
 CC NOTE=Ref.2.
 CC -!- MISCELLANEOUS: IC(50) is 68 +- 6 uM on rNa1.2/beta1 channel.
 CC -!- MISCELLANEOUS: IC(50) is 4.3 +- 0.3 uM on insect sodium channel
 CC para/tipe.
 CC -!- SIMILARITY: Belongs to the huwentoxin-I family.
 CC PDB; INIX; NMR; A=1-33.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0019871; F:sodium channel inhibitor activity; NAS.
 DR GO; GO:0006952; P:defense response; NAS.
 DR GO; GO:0009405; P:pathogenesis; NAS.
 KW 3D-structure; Amidation; Direct protein sequencing;
 KW Ionic channel inhibitor; Neurotoxin; Sodium channel inhibitor; Toxin.
 FT DISULFID 2 17
 FT DISULFID 9 22
 FT DISULFID 16 29
 FT MOD RES 33 33
 SQ SEQUENCE 33 AA; 3614 MW; 24E8E5053A41E377 CRC64;
 Leucine amide.

Query Match 16.7%; Score 34; DB 1; Length 33;
 Best Local Similarity 46.7%; Pred. No. 3.9e+03;
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 7 GKCHCHMGTHCHSSD 21

Db 12 GKNECCSGYACNSRD 26

RESULT 12

Q9WU1 PRELIMINARY; PRT; 33 AA.
 AC Q9WU1; 17 CHSDGPRGVIP 28
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cbl; TISSUE=Cauda epididymis;
 RX MEDLINE=94436209; PubMed=10504302;
 RA Pittocci C., Renzi L., Zaccagnini G., Cimini D., Degraasi F.,
 RA Giordano R., Magnano A.R., Lorenzini R., Lavia P., Spadafora C.;
 RA "A fraction of mouse sperm chromatin is organized in nucleosomal
 RT hypersensitive domains enriched in retroposon.";
 RL J. Cell Sci. 112:3537-3548(1999).
 DR EMBL; AJ133884; CAB41620.1; .
 KW Hypothetical protein.
 FT NON_TER 1 33
 FT NON_TER 33 33
 SQ SEQUENCE 33 AA; 3640 MW; BB79603F69514199 CRC64;

Query Match 16.4%; Score 33.5; DB 2; Length 33;
 Best Local Similarity 35.0%; Pred. No. 4.5e+03;
 Matches 7; Conservative 1; Mismatches 7; Indels 5; Gaps 1;

Qy 14 GTHCHSDGPRGVIPRCP 33

Db 15 GTFTHPQS-----VPPPLCP 29

RESULT 13

Q7PD61 PRELIMINARY; PRT; 23 AA.
 AC Q7PD61; 20 SDGPRGVIPRCP 31
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE (ENSANGP00000023570 (ENSANGP00000022631) (ENSANGP00000022834)
 DE (ENSANGP00000023690) (ENSANGP00000025178) (ENSANGP00000023243)
 DE (ENSANGP00000022360) (ENSANGP00000022693) (ENSANGP00000023784)
 DE (ENSANGP000000224643) (ENSANGP00000024706) (ENSANGP00000024202)
 GN Name=ENSANGG00000020927;
 GN SYNonyms=ENSANGG00000019887, ENSANGG00000019961, ENSANGG00000020021,
 GN ENSANGG00000020103, ENSANGG00000020106, ENSANGG00000020495,
 GN ENSANGG00000020534, ENSANGG00000020760, ENSANGG00000020822,
 GN ENSANGG00000020831, ENSANGG00000020909, ENSANGG00000021110;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
 CX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AA061008987; EAA43057.1; .
 FT NON_TER 1 23
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2377 MW; 5FFB90A0CFIDA684 CRC64;

Query Match 16.2%; Score 33; DB 2; Length 23;
 Best Local Similarity 58.3%; Pred. No. 3.7e+03;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 17 CHSDGPRGVIP 28

Db 11 CHAGD--RGSIP 20

RESULT 14

Q9LJE7 PRELIMINARY; PRT; 26 AA.
 AC Q9LJE7; 15 OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRP15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RA "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP000603; BAB01749.1;
 SQ SEQUENCE 26 AA; 2779 MW; 0B6012415641A588 CRC64;

Query Match 16.2%; Score 33; DB 2; Length 26;
 Best Local Similarity 41.7%; Pred. No. 4.1e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 20 SDGPRGVIPRCP 31

Db 15 SKHPSGIVPTPQ 26

RESULT 15

SCX9_BUTOC STANDARD; PRT; 33 AA.
 AC P04099; 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neurotoxin IX (Fragment).
 OS Buthus occitanus tunetanus (Common European scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthida; Buthoidea; Buthidae; Buthus.
 CX NCBI_TaxID=6871;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=84224814; PubMed=6729843;
 RA Martin M.-F., Rochat H.;
 RA "Purification of thirteen toxins active on mice from the venom of the
 RL North African scorpion Buthus occitanus tunetanus.";
 RL Toxicon 22:279-291(1984).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
 CC Alpha-toxin subfamily.
 DR PIR; A05136; A05136.
 DR HSSP; P45697; ISN1.
 DR InterPro; IPR002061; Scorpion_toxinL.

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OM protein - protein search, using sw model

Run on: November 16, 2004, 22:50:07 ; Search time 149 Seconds
(without alignments)
79.450 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204
Sequence: 1 STVYQKCHCHWTHCHSSDGRGVIPRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 799979

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	33	4	AAE02773 Human Nkp
2	204	100.0	33	8	ADQ30926 Human Nkp
3	52	25.5	31	5	AAM49583 Human bet
4	47	23.0	14	2	AAW67146 Antibody
5	45	22.1	27	7	ADP13180 Human PCS
6	43	21.1	22	2	AAZ28526 Erythrope
7	43	21.1	25	2	AAZ19672 SEQ ID NO
8	43	21.1	29	4	ABG26169 Novel hum
9	42.5	20.8	30	5	ABE88779 Conus str
10	42	20.6	30	4	AAO09316 Human pol
11	42	20.6	30	5	AAU85017 Human GAG
12	41.5	20.3	29	2	AAZ26117 Phospholi
13	41.5	20.3	29	3	AAZ83592 N-termina
14	41	20.1	15	6	ABR54550 Prostate
15	41	20.1	15	7	ADP14409 Human pro
16	41	20.1	15	7	ADG26825 Human pro
17	41	20.1	16	6	AAO23013 Collagen
18	41	20.1	29	6	ABR98386 Tumour ce
19	41	20.1	29	7	ADG84732 MCF-7 bre
20	41	20.1	32	4	AAO13604 Human pol
21	40.5	19.9	30	5	ABE88909 Conus str
22	40.5	19.9	31	8	ADI36928 Human leu
23	40.5	19.9	32	4	AAO12330 Human pol
24	40	19.6	19	4	AAE06236 H-S 19-me
25	40	19.6	19	7	ADF93233 Transport

26	40	19.6	26	8	ADG75335
27	40	19.6	28	3	AAE02773
28	40	19.6	29	3	AAE02773
29	40	19.6	29	6	ADA27069
30	40	19.6	29	8	ADG86601
31	40	19.6	31	3	AAE02773
32	40	19.6	31	6	ADA27077
33	40	19.6	31	8	ADG86609
34	40	19.6	32	4	AAO07747
35	39.5	19.4	6	2	AAW88030
36	39.5	19.4	27	2	AAW06728
37	39.5	19.4	30	5	ABE88902
38	39.5	19.4	30	5	ABE88903
39	39.5	19.4	30	5	ABE88903
40	39.5	19.4	30	5	ABE88903
41	39	19.1	6	2	AAW88029
42	39	19.1	16	3	AAO1589
43	39	19.1	16	5	AAU85716
44	39	19.1	16	6	AAO23009
45	39	19.1	16	7	ABR62081

ALIGNMENTS

RESULT 1

AAE02773
ID AAE02773 standard; peptide; 33 AA.

XX

XX AAE02773;

XX AC

DT 06-AUG-2001 (first entry)

XX

DE Human Nkp30 receptor intracellular region sequence.

XX

KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
KW therapy; intracellular region.

XX

XX Homo sapiens.

OS

PN WO200136630-A2.

XX

XX 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-EP011697.

XX

PR 15-NOV-1999; 99CA-02288307.

XX

PR 15-NOV-1999; 99US-00440514.

XX

PA (INNA-) INNATE PHARMA SAS.

PA

PA (UYGE-) UNIV GENOVA.

XX

PI Moretta A, Bottino C, Biassoni R;

XX

PT Novel compound, useful for detection and/or quantifying the presence of

XX

PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX

PS Claim 1; Fig 7B; 83pp; English.

XX

The invention relates to human Nkp30 receptor and its corresponding cDNA molecule which is involved in natural cytotoxicity mediated by natural killer (NK) cells and antibodies that identify the same. Nkp30 is selectively is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively expressed on the surface of human mature NK cells. Nkp30 and its cDNA are useful for detecting and/or quantifying the presence of NK cells in a biological sample. The invention also provide kits for detecting and/or quantifying the presence of NK cells, for the selective removal of NK cells from a biological sample, for the positive and selective purification of NK cells from a biological sample and for the in vitro

CC stimulation of NK cell cytotoxicity. The invention further provides a
 CC pharmaceutical composition which is used as a drug for grafting
 CC enhancement, graft versus host (GVH) inhibition, stimulation of graft
 CC versus tumour (GVT) and especially graft versus leukaemia (GvL), and for
 CC the prevention, palliation and/or therapy of solid or liquid tumours,
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
 CC microorganism, notably viral infection. Nkp30 antibodies are useful for
 CC identifying Nkp30 natural ligands and allow assessment of the level of
 CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
 CC comparison of this level to the standard physiological one. Hence Nkp30
 CC antibodies are useful in the diagnosis of tumours or of infection. The
 CC present sequence is the intracellular region of human Nkp30 receptor
 CC
 CC Sequence 33 AA;

Query Match 100.0%; Score 204; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33
 DB 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33

RESULT 2

ADQ30926
 ID ADQ30926 standard; protein; 33 AA.

XX
 AC ADQ30926;

DT 23-SEP-2004 (first entry)

XX Human Nkp30 cytoplasmic tail.

DE Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.

XX Homo sapiens.

PN WO2004056392-A1.

PD 08-JUL-2004.

XX 22-DEC-2003; 2003WO-EP014716.

PR 23-DEC-2002; 2002US-0435344P.

XX (INNA-) INNATE PHARMA.

PI Romagne F, Andre P;

XX WPI; 2004-507595/48.

PT Pharmaceutical compositions that stimulate proliferation of natural
 PT killer cells useful for therapy of melanoma, chronic myeloid, and
 PT leukemia, comprise an anti-natural killer cell receptor antibody and
 PT interleukins.

PS Claim 3; SEQ ID NO 4; 35pp; English.

XX The present sequence is that of the cytoplasmic tail of human Nkp30
 CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by
 CC natural killer (NK) cells, and particularly by mature NK cells. Claimed
 CC pharmaceutical compositions that have a stimulating effect on the
 CC proliferation of NK cells comprise an antibody such as an anti-Nkp30
 CC antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
 CC antibody(ies) and cytokine(s) being administered together or separately
 CC to a subject. The anti-Nkp30 antibody is an isolated antibody or its
 CC antigen-binding fragment which specifically binds to Nkp30 or to a
 CC fragment, including the cytoplasmic tail, of Nkp30. The pharmaceutical
 CC compositions, when used for daily subcutaneous injection, comprising from
 CC 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1
 CC million units/square meters/day of cytokine(s), are useful for the

CC prevention, palliation and therapy of e.g. melanoma, chronic myeloid
 CC leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
 CC prevention, palliation and therapy (claimed).

XX Sequence 33 AA;

Query Match 100.0%; Score 204; DB 8; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33
 DB 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33

RESULT 3

AAM49583

ID AAM49583 standard; peptide; 31 AA.

XX
 AC AAM49583;

XX 28-MAY-2002 (first entry)

DE Human beta-defensin hBD-10 peptide fragment #1.

XX Defensin; human; antibacterial; antiinfectivity; contraceptive;
 KW peptide therapy; infection; gastrointestinal; respiratory tract;
 KW urogenital tract; skin; gland; sperm penetration; systemic disease;
 KW infertility; sperm initiation; sperm maturation; diagnostic marker;
 KW inflammatory disease; epithelial organ; gene therapy.

OS Homo sapiens.

XX WO200204487-A2.

PD 17-JAN-2002.

XX 11-JUL-2001; 2001WO-EP007973.

XX 11-JUL-2000; 2000DE-01033505.

XX (IPPP-) IPF PHARM GMBH.

PI Forasmann W, Conejo-Garcia J, Adermann K;

XX WPI; 2002-179697/23.

XX New defensin type peptides useful for treatment of bacterial infections
 PT and for fertility control, and as a diagnostic marker of inflammatory
 PT disease in epithelial organs.

PS Claim 6; Page 22; 41pp; German.

XX This invention describes novel peptides (I) of the defensin type which
 CC have antibacterial, antiinfectivity and contraceptive activity and which
 CC can be used for peptide therapy. (I), and their derivatives and
 CC fragments, are used: (i) to treat bacterial infections, particularly of
 CC the gastrointestinal, respiratory or urogenital tracts, or of the skin
 CC and associated glands; (ii) to treat systemic diseases associated with
 CC overexpression or deficiency of defensin production, particularly as
 CC substitution therapy or by using (I)-specific antibodies; (iii) to treat
 CC infertility, especially where the result of disordered sperm penetration,
 CC initiation or maturation, also as contraceptives; and (iv) as a diagnostic
 CC marker of inflammatory disease in epithelial organs. Both chronic and
 CC acute diseases may be treated, e.g. in intensive care. Also genes that
 CC encode (I) can be used for systemic or localised gene therapy of the
 CC specified diseases, in epithelial tissues or organs. (I) have exceptional
 CC biological activity and since they do not induce an immune response, they
 CC are particularly well suited for long-term use. This sequence represents
 CC a human defensin described in the disclosure of the invention

XX Sequence 31 AA;

DE Erythropoietin receptor (EPO-R) binding peptide.

KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;

KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;

KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;

KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

OS

XX WO9640749-A1.

PN

XX 19-DEC-1996.

PD

XX 07-JUN-1996; 96WO-US009810.

PF

XX 07-JUN-1995; 95US-00484631.

PR

XX 07-JUN-1995; 95US-00484635.

PR

XX (JOHJ) JOHNSON & JOHNSON CORP.

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;

PI Johnson D, Mulcahy L;

PI

XX WPI; 1997-052225/05.

DR

XX Erythropoietin receptor binding peptide - useful for treating disorders

PT characterised by deficiency of EPO, or low or defective red blood cell

PT population.

PT

XX Disclosure; Page 25; 95pp; English.

PS

XX The invention describes a peptide of 10-40 amino acid residues which

CC binds to erythropoietin (EPO) receptor and which includes the amino acid

CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,

CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically

CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,

CC the peptide may be cyclised or dimerised. The peptide can be used to

CC treat a patient having a disorder characterised by a deficiency of EPO or

CC a low or defective red blood cell population. It can be used to treat end

CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune

CC disease, chronic inflammatory diseases or malignancy; beta-thalassaemia;

CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute

CC blood loss; aging; and neoplastic disease states accompanied by abnormal

CC erythropoiesis. The peptides can also be used as reagents for detecting

CC EPO receptors on living cells, in biological fluids, in tissue

CC homogenates, etc. Sequences AAY26352-548 are representative peptides

CC falling within the above peptide motif and isolated during the affinity

CC selection process

XX

SQ Sequence 22 AA;

Query Match 21.1%; Score 43; DB 2; Length 22;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;

Matches 7; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 10 HCHMGTHCHSSDGP 23

DB 6 HCHMGPTWCHGP 19

|||||

RESULT 7

AAAY19672

ID AAY19672 standard; protein; 25 AA.

XX

XX AAY19672;

AC

XX 14-JUL-1999 (first entry)

DT

XX SEQ ID NO 390 from WO9922243.

DE

XX Human secreted protein; cancer; tumour; neurodegenerative disorder;

KW developmental abnormality; fetal deficiency; blood disorder; leukemia;

KW

KW immune system disease; autoimmune disease; hepatic disease;

KW renal disease; lymphoma; inflammation; allergy; ischemic shock;

KW Alzheimer's; cognitive disorder; schizophrenia; prostate disease;

KW obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease;

KW lung disease; thymus disease; digestive disorder; endocrine disorder;

KW infection; AIDS.

XX

OS Homo sapiens.

XX WO9922243-A1.

PN

XX 06-MAY-1999.

PD

XX 23-OCT-1998; 98WO-US022376.

PF

XX 24-OCT-1997; 97US-0062784P.

PR

XX 24-OCT-1997; 97US-0063088P.

PR

XX 24-OCT-1997; 97US-0063089P.

PR

XX 24-OCT-1997; 97US-0063090P.

PR

XX 24-OCT-1997; 97US-0063091P.

PR

XX 24-OCT-1997; 97US-0063092P.

PR

XX 24-OCT-1997; 97US-0063097P.

PR

XX 24-OCT-1997; 97US-0063098P.

PR

XX 24-OCT-1997; 97US-0063099P.

PR

XX 24-OCT-1997; 97US-0063100P.

PR

XX 24-OCT-1997; 97US-0063101P.

PR

XX 24-OCT-1997; 97US-0063109P.

PR

XX 24-OCT-1997; 97US-0063110P.

PR

XX 24-OCT-1997; 97US-0063111P.

PR

XX 24-OCT-1997; 97US-0063148P.

PR

XX 24-OCT-1997; 97US-0063386P.

PR

XX 24-OCT-1997; 97US-0063387P.

PR

XX (HUMA-) HUMAN GENOME SCI INC.

PA

XX Feng P, Rosen CA, Ruben SM, Ni J, Wei Y, Soppet DR, Moore PA;

PI Kayw H, Lafleur DW, Olsen HS, Brewer LA, Shi Y, Ebner R, Young P;

PI Greene JM, Florence KA, Florence C, Duan DR, Janat F, Endress GA;

PI Carter KC;

PI

XX WPI; 1999-303069/25.

DR

XX New isolated human genes and the secreted polypeptides they encode.

PT

XX Disclosure; Page 492; 546pp; English.

PS

XX The specification describes human secreted proteins. The polynucleotides

CC and their corresponding secreted polypeptides are useful for preventing,

CC treating or ameliorating medical conditions, e.g. by protein or gene

CC therapy. Pathological conditions can also be diagnosed by determining the

CC amount of the polypeptides in a sample or by determining the presence of

CC mutations in the polynucleotides. Specific uses are described for each of

CC the polynucleotides, based on which tissues they are most highly

CC expressed in, and include developing products for the diagnosis or

CC treatment of cancer, tumours, neurodegenerative disorders, developmental

CC abnormalities and fetal deficiencies, blood disorders, leukemias,

CC diseases of the immune system, autoimmune diseases, hepatic and renal

CC disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's

CC and cognitive disorders, schizophrenia, prostate diseases, obesity,

CC disorders involving osteoclasts such as osteoporosis, arthritis or

CC malignancies, diseases of testes, lung or thymus, digestive/endocrine

CC disorders, infections and AIDS. The polypeptides are also useful for

CC identifying their binding partners

XX

SQ Sequence 25 AA;

Query Match 21.1%; Score 43; DB 2; Length 25;

Best Local Similarity 54.5%; Pred. No. 3.5e+02;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 PRGVIPPEPCP 33

DB 2 PRALVPRPCP 12

|||||


```

XX SQ Sequence 30 AA;
Query Match 20.8%; Score 42.5; DB 5; Length 30;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 9 CHCHMGTHCHSSDGRGV 26
DB 1 CH-HXGLXCSSDDGCCGM 17

RESULT 10
AAO09316
ID AAO09316 standard; protein; 30 AA.
XX AC AAO09316;
XX OS Homo sapiens.
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 23208.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX DR N-PSDB; AAI89247.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX FS Claim 20; SEQ ID NO 23208; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 30 AA;
Query Match 20.6%; Score 42; DB 4; Length 30;
Best Local Similarity 40.0%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 10 HCHMGTHCHSSDGRGV 29
DB 2 HTHHTHTHSHTHSHLPE 21

RESULT 11
AAU85017
ID AAU85017 standard; peptide; 30 AA.
XX AC AAU85017;
XX DT 08-MAY-2002 (first entry)
XX DE Human GAGE-1 segment 6.
XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX KW viral infection; human immunodeficiency virus; melanoma;
XX KW bacterial infection; Salmonella; Legionella; parasitic infection;
XX KW Trypanosoma; Toxoplasma; Giardia.
XX OS Homo sapiens.
XX PN WO200190197-A1.
XX PD 29-NOV-2001.
XX PF 25-MAY-2001; 2001WO-AU000622.
XX PR 26-MAY-2000; 2000AU-00007761.
XX PA (AUSU) UNIV AUSTRALIAN NAT.
XX PI Thomson SA, Ramshaw IA;
XX WPI; 2002-147575/19.
XX DR N-PSDB; ABK36937.
XX PT New synthetic polypeptides having several different segments of at least
XX PT one parent polypeptide linked together differently compared to the
XX PT linkage in the parent polypeptide, for inducing immune response against a
XX PT pathogen or cancer.
XX PS Example 3; Fig 27; 364pp; English.
XX CC The invention relates to a new synthetic polypeptide (I) comprising
XX CC several different segments of at least one parent polypeptide linked
XX CC together in a different relationship relative to their linkage in the
XX CC parent polypeptide to impede, abrogate or otherwise alter at least one
XX CC function associated with the parent polypeptide and for inducing an
XX CC immune response against a pathogen or cancer. Also included are a
XX CC synthetic polynucleotide encoding and a computer system for designing the
XX CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX CC are referred to as a Savine. The synthetic polypeptide is useful for
XX CC modulating immune responses preferably directed against a pathogen or a
XX CC cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX CC oesophagus, brain, testicle, uterus), as potentiating agents.
XX CC Compositions comprising the polypeptide may be used in the treatment or
XX CC prophylaxis against viral (such as infections caused by HIV (human
XX CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic.
XX CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX CC a peptide derived from a parent protein used to construct a savine of the
XX CC invention
XX SQ Sequence 30 AA;
Query Match 20.6%; Score 42; DB 5; Length 30;
Best Local Similarity 40.9%; Pred. No. 5.6e+02;
Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 12 HMGTHCHSSDGRGV 33
DB 12 HMGTHCHSSDGRGV 33

```


Db 7 HPQTGCECEDGPDGMDFPAP 28

RESULT 12
AAY26117
ID AAY26117 standard; peptide; 29 AA.
AC AAY26117;
XX
XX
DE 22-OCT-1999 (first entry)
XX
XX AAY26117;
XX
XX
DT 22-OCT-1999 (first entry)
XX
XX
DE Phospholipase A2 inhibitor-NAI alpha iN.
XX
XX Phospholipase A2 inhibitor; PLA2 inhibitor; NAI alpha iN; alpha chain;
KW anti-inflammatory activity; recombinant PLA2 inhibitor; prophylactic;
KW therapeutic application; rheumatoid arthritis; osteoarthritis; asthma;
KW allergic reaction; psoriasis; multiple organ failure; acute pancreatitis;
KW acute lung failure; septic shock; adult respiratory distress syndrome;
KW toxin.
XX
XX Notechis ater.
OS
XX WO9929726-A1.
PN
XX 17-JUN-1999.
PD
XX 30-NOV-1998; 98WO-AU000992.
PF
XX 05-DEC-1997; 97AU-00000767.
FR
XX (HSCP-) HSC PLA PTY LTD.
PA
XX (FLAIR-) FLAIR PLA R & D PTY LTD.
PA
XX (ACTI-) ACTIVE PLA R & D PTY LTD.
PA
XX (HERA-) HERACLES PLA R & D PTY LTD.
PA
XX (APEL-) APEDA PLA R & D PTY LTD.
PA
XX (EDZE-) EDZELL PLA R & D PTY LTD.
PA
XX (NORT-) NORTHMOOR PLA R & D PTY LTD.
XX
XX Broady KW, Hains PG;
PI
XX WPI; 1999-385577/32.
DR
XX Broad-spectrum phospholipase A2 inhibitor derived from snake venom.
PT
XX Claim 10; Page 85; 161pp; English.
XX
XX The present sequence is that of NAI alpha iN peptide. NAI alpha iN is a
CC broad-spectrum phospholipase A2 (PLA2) inhibitor. It comprises N-terminal
CC region of alpha-chain from isoform I of PLA2 inhibitor isolated from
CC Notechis ater. It is capable of inhibiting two or more of PLA2 type I, II
CC and/or III enzymes. The PLA2 inhibitor has anti-inflammatory activity.
CC The isolated PLA2 inhibitor or recombinant PLA2 inhibitor are useful in a
CC wide range of prophylactic and therapeutic applications. The
CC phospholipase inhibitors are useful for the treatment of the
CC phospholipase-related symptom(s) of rheumatoid arthritis, osteoarthritis,
CC asthma, allergic reaction, psoriasis, multiple organ failure, acute
CC pancreatitis, acute lung failure, septic shock, adult respiratory
CC distress syndrome or the toxic effects of toxins (e.g. due to insect
CC bites) in humans or animals
XX
XX Sequence 29 AA;

Query Match 20.3%; Score 41.5; DB 2; Length 29;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 8; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

Qy 9 CHCHMGTHCHSSDGRGVIPPEPC 32
Db 6 CH-NFGKDCQSDAEBCASPEDQC 28

RESULT 13
AAY83592
ID AAY83592 standard; peptide; 29 AA.
AC AAY83592;
XX
XX
DE 29-AUG-2000 (first entry)
XX
XX N-terminal fragment of NAI PLA_2 inhibitor alpha chain (isoform 1).
XX
XX Phospholipase; inhibitor; inhibition; COX1; COX2; cyclooxygenase; cancer;
KW treatment; inflammation; cytokine; NSAID; prostaglandin; non-steroidal;
KW anti-inflammatory; arachidonic acid; isoform.
XX
XX Notechis ater.
OS
XX WO200028997-A1.
PN
XX 25-MAY-2000.
PD
XX 12-NOV-1999; 99WO-AU001004.
PF
XX 12-NOV-1998; 98US-0108254P.
PR
XX (ANAL-) ANALYTICA LTD.
PA
XX Tseng APS, Broady KW;
PI
XX WPI; 2000-387605/33.
DR
XX Use of phospholipase inhibitors for prophylaxis and treatment of cancer
PT in human, primate, livestock animal or avian species.
XX
XX Claim 8; Page 81; 107pp; English.
XX
XX Inhibitors of phospholipase activity, in particular phospholipase A2
CC (PLA2) can be used for controlling the growth and/or development of
CC cancer in an animal. The use of phospholipase inhibitors provides an
CC alternative to the use of non-steroidal anti-inflammatory drugs (NSAIDs)
CC since prolonged use of these compounds can lead to adverse
CC gastrointestinal side effects. Most NSAIDs do not discriminate between
CC the two isoforms of cyclooxygenase (COX1, COX2). COX1 is constitutively
CC expressed in a number of cells whereas COX2 is inducible by e.g. growth
CC factors and cytokines. COX2 does therefore have a role to play in
CC inflammation. Inhibition of secretory PLA2 reduces expression of one
CC isoform of cyclooxygenase (COX2) and reduces catalytic conversion of
CC arachidonic acid to prostaglandin
XX
XX Sequence 29 AA;

Query Match 20.3%; Score 41.5; DB 3; Length 29;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 8; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

Qy 9 CHCHMGTHCHSSDGRGVIPPEPC 32
Db 6 CH-NFGKDCQSDAEBCASPEDQC 28

RESULT 14
ABR54550
ID ABR54550 standard; protein; 15 AA.
XX
XX ABR54550;
AC
XX
XX
DT 28-AUG-2003 (first entry)
XX
XX Prostate tumour specific protein SEQ ID 959.
DE
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer.
KW
XX Homo sapiens.
OS
XX WO200289747-A2.
PN

Db 7 HPQTGCECEDGPDQGMDFPAP 28

RESULT 12
AAY26117

ID AAY26117 standard; peptide; 29 AA.
AC AAY26117;
XX
XX
DE 22-OCT-1999 (first entry)
XX
XX AAY26117;
AC
XX
DT 22-OCT-1999 (first entry)
XX
XX Phospholipase A2 inhibitor-NAI alpha iN.
DE
XX Phospholipase A2 inhibitor; PLA2 inhibitor; NAI alpha iN; alpha chain;
KW anti-inflammatory activity; recombinant PLA2 inhibitor; prophylactic;
KW therapeutic application; rheumatoid arthritis; osteoarthritis; asthma;
KW allergic reaction; psoriasis; multiple organ failure; acute pancreatitis;
KW acute lung failure; septic shock; adult respiratory distress syndrome;
KW toxin.
KW
XX
XX Notechis ater.
OS
XX WO9929726-A1.
PN
XX 17-JUN-1999.
PD
XX 30-NOV-1998; 98WO-AU000992.
PF
XX 05-DEC-1997; 97AU-00000767.
FR
XX {HSCP-} HSC PLA PTY LTD.
PA
XX {FLAIR-} FLAIR PLA R & D PTY LTD.
PA
XX {ACTI-} ACTIVE PLA R & D PTY LTD.
PA
XX {HERA-} HERACLES PLA R & D PTY LTD.
PA
XX {APEL-} APEDA PLA R & D PTY LTD.
PA
XX {EDZE-} EDZELL PLA R & D PTY LTD.
PA
XX {NORT-} NORTHMOOR PLA R & D PTY LTD.
PA
XX Broady KW, Hains PG;
PI
XX WPI; 1999-385577/32.
DR
XX Broad-spectrum phospholipase A2 inhibitor derived from snake venom.
PT
XX Claim 10; Page 85; 161pp; English.
XX The present sequence is that of NAI alpha in peptide. NAI alpha iN is a
CC broad-spectrum phospholipase A2 (PLA2) inhibitor. It comprises N-terminal
CC region of alpha-chain from isoform I of PLA2 inhibitor isolated from
CC Notechis ater. It is capable of inhibiting two or more of PLA2 type I, II
CC and/or III enzymes. The PLA2 inhibitor has anti-inflammatory activity.
CC The isolated PLA2 inhibitor or recombinant PLA2 inhibitor are useful in a
CC wide range of prophylactic and therapeutic applications. The
CC phospholipase inhibitors are useful for the treatment of the
CC phospholipase-related symptom(s) of rheumatoid arthritis, osteoarthritis,
CC asthma, allergic reaction, psoriasis, multiple organ failure, acute
CC pancreatitis, acute lung failure, septic shock, adult respiratory
CC distress syndrome or the toxic effects of toxins (e.g. due to insect
CC bites) in humans or animals
XX
XX Sequence 29 AA;
XX Query Match 20.3%; Score 41.5; DB 2; Length 29;
XX Best Local Similarity 33.3%; Pred. No. 6.3e+02;
XX Matches 8; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 9 CHCHMGTHCHSSDGRGVIPPEPC 32
DB 6 CH-NFGKDCQSDAEBCASPEDQC 28

RESULT 13
AAY83592

ID AAY83592 standard; peptide; 29 AA.
AC AAY83592;
XX
XX 29-AUG-2000 (first entry)
DE
XX N-terminal fragment of NAI PLA_2 inhibitor alpha chain (isoform 1).
XX
XX Phospholipase; inhibitor; inhibition; COX1; COX2; cyclooxygenase; cancer;
KW treatment; inflammation; cytokine; NSAID; prostaglandin; non-steroidal;
KW anti-inflammatory; arachidonic acid; isoform.
KW
XX Notechis ater.
OS
XX WO200028997-A1.
PN
XX 25-MAY-2000.
PD
XX 12-NOV-1999; 99WO-AU001004.
PF
XX 12-NOV-1998; 98US-0108254P.
PR
XX (ANAL-) ANALYTICA LTD.
PA
XX Tseng APS, Broady KW;
PI
XX WPI; 2000-387605/33.
DR
XX Use of phospholipase inhibitors for prophylaxis and treatment of cancer
PT in human, primate, livestock animal or avian species.
XX Claim 8; Page 81; 107pp; English.
XX Inhibitors of phospholipase activity, in particular phospholipase A₂
CC (PLA₂) can be used for controlling the growth and/or development of
CC cancer in an animal. The use of phospholipase inhibitors provides an
CC alternative to the use of non-steroidal anti-inflammatory drugs (NSAIDs)
CC since prolonged use of these compounds can lead to adverse
CC gastrointestinal side effects. Most NSAIDs do not discriminate between
CC the two isoforms of cyclooxygenase (COX1, COX2). COX1 is constitutively
CC expressed in a number of cells whereas COX2 is inducible by e.g. growth
CC factors and cytokines. COX2 does therefore have a role to play in
CC inflammation. Inhibition of secretory PLA₂ reduces expression of one
CC isoform of cyclooxygenase (COX2) and reduces catalytic conversion of
CC arachidonic acid to prostaglandin
XX
XX Sequence 29 AA;
XX Query Match 20.3%; Score 41.5; DB 3; Length 29;
XX Best Local Similarity 33.3%; Pred. No. 6.3e+02;
XX Matches 8; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 9 CHCHMGTHCHSSDGRGVIPPEPC 32
DB 6 CH-NFGKDCQSDAEBCASPEDQC 28

RESULT 14
ABR54550

ID ABR54550 standard; protein; 15 AA.
XX
XX ABR54550;
AC
XX 28-AUG-2003 (first entry)
DT
XX Prostate tumour specific protein SEQ ID 959.
DE
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer.
KW
XX Homo sapiens.
OS
XX WO200289747-A2.
PN

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XX PD 14-NOV-2002.
XX PF 09-MAY-2002; 2002WO-US014753.
XX PF 09-MAY-2001; 2001US-00852911.
XX PR 29-JUN-2001; 2001US-00895814.
XX PR 10-DEC-2001; 2001US-00012896.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Bassolac, Foy TW, Watanabe Y;
PI Deng T;
XX PR 2003-167130/16.
XX DR WPI;
XX PR New prostate-specific proteins and genes, useful in gene therapy,
XX particularly for stimulating an immune response in a patient, or treating
XX prostate cancer in a patient, as well as for diagnosing prostate cancer
XX in a patient.
XX PS Claim 2; Page 655; 691pp; English.
XX CC The present invention relates to novel prostate-specific proteins (PSP)
XX and their coding sequences. The PSPs and their coding sequences are
XX useful for stimulating an immune response in a patient, or for treating
XX prostate cancer in a patient and for determining, detecting or diagnosing
XX the presence of a cancer in a patient. The present sequence was used to
XX illustrate the invention
XX SQ Sequence 15 AA;
Query Match 20.1%; Score 41; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 15 THCHSSDQPR 24
DQ 5 THCHTTGTR 14
RESULT 15
ADBI4409
ID ADBI4409 standard; peptide; 15 AA.
XX AC ADBI4409;
XX DT 18-DEC-2003 (first entry)
XX DX Human prostate specific protein P77SP peptide #3.
XX DE Human, prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
XX cell therapy; vaccine; T-cell epitope;
XX KW Class I major histocompatibility complex allele; MHC; prostate cancer;
XX tumour; antigen presenting cell; epitope.
XX OS Homo sapiens.
XX PN US2003185830-A1.
XX PD 02-OCT-2003.
XX PF 12-NOV-2002; 2002US-00294025.
XX PR 25-FEB-1997; 97US-00806099.
XX PR 01-AUG-1997; 97US-00904804.
XX PR 09-FEB-1998; 98US-00020956.
XX PR 25-FEB-1998; 98US-00030607.
XX PR 14-JUL-1998; 98US-00115453.
XX PR 23-SEP-1998; 98US-00159812.

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PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593733.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759443.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX (CORI-) CORIXA CORP.
XX PI Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX DR New isolated polypeptide for use in a vaccine for stimulating an immune
XX response, or for treating or diagnosis cancer, preferably prostate
XX cancer.
XX PS Example 18; Page: 101pp; English.
XX CC The invention relates to an isolated polypeptide comprising no more than
XX 11542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
XX peptides comprise a fragment ADBI3563 of that contain naturally processed
XX T-cell epitopes for 3 class I major histocompatibility complex (MHC)
XX alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
XX cDNA, one of 648 disclosed as new. Also included are nucleic acids
XX encoding the proteins and peptides, expression vectors, a host cell
XX transformed with the vector, an isolated antibody (or antigen binding
XX fragment) that specifically binds to the protein or peptide, detecting
XX the presence of a cancer in a patient (comprising contacting a patient
XX sample with a binding agent that binds to the peptides or a polypeptide
XX appearing as ADBI3563, detecting the amount of polypeptide that binds to
XX the agent and comparing the amount of polypeptide to a predetermined cut-
XX off value to determine the presence of cancer), a fusion protein
XX comprising the peptides or proteins, stimulating or expanding T cells
XX specific for a tumour protein comprising contacting T cells with the
XX peptides or the isolated T cell population, treating prostate cancer in a
XX patient comprising administering a composition comprising the peptides,
XX nucleic acids, antibodies or compounds, determining the presence of a
XX cancer in a patient and treating prostate cancer in a patient comprising
XX incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
XX from a patient with the peptides or antigen presenting cells that express
XX the peptides so that the T cells proliferate, and administering the
XX proliferated T cells to the patient. The peptides (or an oligonucleotide
XX that hybridises to nucleic acid encoding them), is used to detect the
XX presence of cancer in a patient. The peptides, nucleic acids encoding, or
XX antigen-presenting cells expressing the nucleic acid, are used to
XX stimulate or expand T cells specific for a tumour protein. The peptides,
XX nucleic acids, antibodies, fusion proteins, T cell populations or antigen
XX presenting cells are used to stimulate an immune response or treat
XX prostate cancer in a patient. The present sequence is an epitope or
XX peptide derived from one of the prostate specific proteins of the
XX invention. Note: Except where otherwise indicated, the sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030185830.

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SQ Sequence 15 AA;
Query Match      20.1%; Score 41; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. NO. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 15 THCHSSDGPR 24
   |||::|
Db 5 THCHTTGTR 14

Search completed: November 16, 2004, 23:04:10
Job time : 152 secs
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 23:07:28 ; Search time 135 Seconds
(without alignments)
86.489 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHCHMGTHCHSSDGRGVIPERPCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 segs, 353819137 residues

Total number of hits satisfying chosen parameters: 333260

Minimum DB seq length: 0

Maximum DB seq length: 33

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

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9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*

10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*

11: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*

12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*

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20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	33	13	US-10-036-444-6
2	52	25.5	31	16	US-10-332-765-5
3	43	21.1	25	14	US-10-231-417-437
4	42.5	20.8	30	9	US-09-894-882-345
5	42	20.6	30	15	US-10-296-734-1228
6	41	20.1	15	9	US-09-895-814-959
7	41	20.1	15	13	US-10-012-896-959
8	41	20.1	15	14	US-10-144-678A-959
9	41	20.1	15	14	US-10-294-025-959
10	41	20.1	20	10	US-09-974-026-15
11	41	20.1	29	14	US-10-199-820-264
12	41	20.1	32	16	US-10-767-701-59248
13	40.5	19.9	30	9	US-09-894-882-481

14	40.5	19.9	31	14	US-10-424-233-27	Sequence 27, Appl
15	40	19.6	19	14	US-10-018-103A-11	Sequence 11, Appl
16	40	19.6	19	14	US-10-131-909A-11	Sequence 11, Appl
17	40	19.6	29	10	US-09-984-130-52	Sequence 52, Appl
18	40	19.6	29	10	US-09-836-353A-52	Sequence 52, Appl
19	40	19.6	31	10	US-09-984-130-60	Sequence 60, Appl
20	40	19.6	31	10	US-09-836-353A-60	Sequence 60, Appl
21	39.5	19.4	30	9	US-09-894-882-471	Sequence 471, Appl
22	39.5	19.4	30	9	US-09-894-882-474	Sequence 474, Appl
23	39.5	19.4	30	9	US-09-894-882-475	Sequence 475, Appl
24	39.5	19.4	32	17	US-10-425-115-249188	Sequence 249188,
25	39	19.1	16	14	US-10-325-021-21	Sequence 21, Appl
26	39	19.1	16	14	US-10-297-229-60	Sequence 60, Appl
27	39	19.1	16	14	US-10-125-869A-148	Sequence 148, Appl
28	39	19.1	23	15	US-10-462-262-372	Sequence 372, Appl
29	39	19.1	23	17	US-10-425-115-239345	Sequence 239345,
30	39	19.1	27	14	US-10-106-698-7657	Sequence 7657, Ap
31	39	19.1	30	13	US-10-127-318-8	Sequence 8, Appli
32	39	19.1	32	9	US-09-864-761-36152	Sequence 36152, A
33	38.5	18.9	19	14	US-10-378-557-53	Sequence 53, Appl
34	38.5	18.9	27	15	US-10-038-854-379	Sequence 379, App
35	38	18.6	30	15	US-10-424-599-186038	Sequence 186038,
36	37.5	18.4	14	13	US-10-004-381-32	Sequence 32, Appl
37	37.5	18.4	32	8	US-08-424-550B-293	Sequence 293, App
38	37.5	18.4	33	14	US-10-105-232-385	Sequence 385, App
39	37.5	18.4	33	14	US-10-189-437-372	Sequence 372, App
40	37	18.1	18	14	US-10-325-567A-959	Sequence 959, App
41	37	18.1	28	15	US-10-038-854-375	Sequence 375, App
42	37	18.1	28	15	US-10-038-854-387	Sequence 387, App
43	37	18.1	29	10	US-09-847-208-125	Sequence 125, App
44	37	18.1	30	11	US-09-978-360A-512	Sequence 512, App
45	36.5	17.9	23	9	US-09-843-676-208	Sequence 208, App

ALIGNMENTS

RESULT 1

US-10-036-444-6
; Sequence 6, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-FR-1060
; CURRENT APPLICATION NUMBER: US/10/036.444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-6

Query Match 100.0%; Score 204; DB 13; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.4e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSSDGRGVIPERPCP 33

DB 1 STVYQKCHCHMGTHCHSSDGRGVIPERPCP 33

RESULT 2

US-10-332-765-5

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; Sequence 5, Application US/10332765
; Publication No. US20040116652A1
; GENERAL INFORMATION:
; APPLICANT: Fortsmann, Wolf-Georg
; APPLICANT: Conejo-Garcia, Jose-Ramon
; APPLICANT: Agermann, Knut
; TITLE OF INVENTION: Method for Producing and Using Novel Human Defensins as Biological
; TITLE OF INVENTION: Active Proteins for Treating Infections and other Illnesses
; FILE REFERENCE: 022584us
; CURRENT APPLICATION NUMBER: US/10/332,765
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: DE10033505.5
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-765-5

Query Match      25.5%; Score 52; DB 16; Length 31;
Best Local Similarity 36.7%; Pred. No. 49;
Matches 11; Conservative 3; Mismatches 10; Indels 6; Gaps 2;

Qy 9 CHCHMGT----HCHSSDGRGVPEP--RC 32
Db 1 CHMQQGCRLFFCHSGKRGICSDPNRC 30

RESULT 3
US-10-231-417-437
; Sequence 437, Application US/10231417
; Publication No. US20030176881A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: P2019P1
; CURRENT APPLICATION NUMBER: US/10/231,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 437
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-417-437

Query Match      21.1%; Score 43; DB 14; Length 25;
Best Local Similarity 54.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 23 PRGVIPPRCP 33
Db 2 PRALVPRCP 12

RESULT 4
US-09-894-882-345
; Sequence 345, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.

; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 345
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus striolatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue3 4 and 18
; OTHER INFORMATION: is Glu or gamma-carboxy-Gl
US-09-894-882-345

Query Match      20.8%; Score 42.5; DB 9; Length 30;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 9 CHCHMGTCHSSDGRGV 26
Db 1 CH-HXGLXCSDSDGCCGM 17

RESULT 5
US-10-296-734-1228
; Sequence 1228, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1228
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: GAGE-1 segment 6
US-10-296-734-1228

Query Match      20.6%; Score 42; DB 15; Length 30;
Best Local Similarity 40.9%; Pred. No. 6.9e+02;
Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 12 HMGTHCHSSDGRGVIPRCP 33
Db 7 HPQTGCSCEDGPDGQEMDPNP 28

RESULT 6
US-09-895-814-959
; Sequence 959, Application US/09895814
; Publication No. US20020193296A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 959
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-814-959

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Query Match      20.1%; Score 41; DB 9; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      15 THCHSSDGPR 24
Db      5 THCHTTTGR 14

```

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RESULT 7
US-10-012-896-959
; Sequence 959, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro

```

```

; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 959
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-959

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Query Match      20.1%; Score 41; DB 13; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      15 THCHSSDGPR 24
Db      5 THCHTTTGR 14

```

```

RESULT 8
US-10-144-678A-959
; Sequence 959, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 959
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-959

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```

Query Match      20.1%; Score 41; DB 14; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      15 THCHSSDGPR 24
Db      5 THCHTTTGR 14

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RESULT 9
US-10-294-025-959
; Sequence 959, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 959
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-959

Query Match 20.1%; Score 41; DB 14; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 15 THCHSSDQGR 24
|||||:|
DB 5 THCHTTGTR 14

RESULT 10
US-09-974-026-15
; Sequence 15, Application US/09974026
; Publication No. US20030194398A1
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P
; APPLICANT: Davis, Gary
; APPLICANT: Delaria, Katherine A
; APPLICANT: Christopher, Marlor W
; APPLICANT: Daniel, Muller K
; TITLE OF INVENTION: Human Bikunin
; FILE REFERENCE: 96-223-ZZ
; CURRENT APPLICATION NUMBER: US/09/974,026
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 09/144,428
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: PCT/US97/03894
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 08/725,251
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US 60/019,793
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: US 60/013,106
; PRIOR FILING DATE: 1996-03-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-026-15

Query Match 20.1%; Score 41; DB 10; Length 20;
Best Local Similarity 53.8%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
QY 6 QGKCHCHMGTHCH 18
|||||:|
DB 9 QEMCHCH--RECH 19

RESULT 11

US-10-199-820-264
; Sequence 264, Application US/10199820
; Publication No. US20030180739A1
; GENERAL INFORMATION:
; APPLICANT: Board of Trustees of the University of Illinois
; APPLICANT: Primiano, Thomas
; APPLICANT: Chang, Bey-dih
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating Ca
; FILE REFERENCE: 99,216-U
; CURRENT APPLICATION NUMBER: US/10/199,820
; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 264
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-820-264

Query Match 20.1%; Score 41; DB 14; Length 29;
Best Local Similarity 31.8%; Pred. No. 8.8e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 8; Gaps 1;
QY 7 GKCHC-----HMGTHCHSS 20
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DB 3 GECHGCKCHAGYIGDNCNC 24

RESULT 12
US-10-767-701-59248
; Sequence 59248, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 59248
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 7217989.pep
US-10-767-701-59248

Query Match 20.1%; Score 41; DB 16; Length 32;
Best Local Similarity 38.5%; Pred. No. 9.6e+02;
Matches 10; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
QY 3 VVYQKCHCHMGTHCHSSDGRGVIP 28
| | | | |
DB 9 VINNGSMCKAG--CSGDDAPRAVFP 32

RESULT 13
US-09-894-882-481
; Sequence 481, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren


```

; PRIOR APPLICATION NUMBER: US 60/173576
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US00/34603
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-018-103A-11

Query Match          19.6%; Score 40; DB 14; Length 19;
Best Local Similarity 60.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      10 HCHMGTHCHS 19
      |||||:||||
Db       6 HSHGSHSHS 15

Search completed: November 16, 2004, 23:19:19
Job time : 137 secs

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Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 23:01:43 ; Search time 38 Seconds
(without alignments)
57.592 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204
Sequence: 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 230622

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Issued Patents, AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	21.8	19	1	US-08-179-481-103
2	43	21.1	22	1	US-08-484-635-166
3	43	21.1	22	2	US-08-484-631-166
4	43	21.1	22	2	US-08-827-570-166
5	42.5	20.8	30	4	US-09-894-882-345
6	40.5	19.9	30	4	US-09-894-882-481
7	39.5	19.4	27	3	US-08-467-822-1
8	39.5	19.4	27	3	US-08-432-597-1
9	39.5	19.4	27	3	US-08-466-248-1
10	39.5	19.4	30	4	US-09-894-882-471
11	39.5	19.4	30	4	US-09-894-882-474
12	39.5	19.4	30	4	US-09-894-882-475
13	39	19.1	30	3	US-09-511-023-8
14	38.5	18.9	31	1	US-07-930-649-12
15	38.5	18.9	31	1	US-08-486-013-9
16	38.5	18.9	31	2	US-08-482-279-9
17	38.5	18.9	31	2	US-08-342-268-9
18	38.5	18.9	31	3	US-09-015-968-9
19	38.5	18.9	31	3	US-09-397-386-9
20	38.5	18.9	31	5	PCT-US93-05235-12
21	38.5	18.9	32	1	US-08-486-013-12
22	38.5	18.9	32	2	US-08-482-279-12
23	38.5	18.9	32	2	US-08-342-268-12
24	38.5	18.9	32	3	US-09-015-968-12
25	38.5	18.9	32	3	US-09-397-386-12
26	38	18.6	19	4	US-09-693-822B-12
27	38	18.6	19	4	US-09-693-822B-14

Sequence 293, App
Sequence 293, App
Sequence 293, App
Sequence 293, App
Sequence 26, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 208, App
Sequence 327, App
Sequence 208, App
Sequence 327, App
Sequence 327, App
Sequence 10, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-179-481-103
; Sequence 103, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
; APPLICANT: CARRAWAY, KERMIT L.
; APPLICANT: CAROTHERS CARRAWAY, CORALIE A.
; APPLICANT: FREGIEN, NEVIS L.
; TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DAREY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,481
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,521
; FILING DATE: 30-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-179-481-103

Query Match 21.8%; Score 44.5; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-166

Query Match 21.1%; Score 43; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 7; Indels 7; Gaps 0;

Qy 10 HCHMGTHCHSSDGP 23
Db 6 HCHMGPTWECHGP 19

RESULT 5
US-09-894-882-345
; Sequence 345, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 345
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus striolatus

FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue3 4 and 18
; OTHER INFORMATION: is Glu or gamma-carboxy-Gl
US-09-894-882-345

Query Match 20.8%; Score 42.5; DB 4; Length 30;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 9 CHCHMGTHCHSSDGPGRV 26
Db 1 CH-HXGLXCSSDDGCCGM 17

RESULT 6
US-09-894-882-481
; Sequence 481, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 481
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus striolatus
US-09-894-882-481

Query Match 19.9%; Score 40.5; DB 4; Length 30;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 9 CHCHMGTHCHSSDGPGRV 26
Db 1 CH-HEGLPCSSDDGCCGM 17

RESULT 7
US-08-467-822-1
; Sequence 1, Application US/08467822
; Patent No. 5843460
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauerbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thiberge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

;; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
;; NUMBER OF SEQUENCES: 44
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; ADDRESSEE: Dunner
;; STREET: 1300 I Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,822
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/447,177
;; FILING DATE: 19-MAY-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/432,697
;; FILING DATE: 02-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03495.0137-02000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4400
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-467-822-1

Query Match 19.4%; Score 39.5; DB 2; Length 27;
Best Local Similarity 58.3%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 7 GKCHCHMGTHCH 18
Db 1 GSC-CHTGNHHD 11

RESULT 8
US-08-432-697-1
; Sequence 1, Application US/08432697
; Patent No. 6248330
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauerbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thiberge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.

;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/432,697
;; FILING DATE: 02-MAY-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03495.0137-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-432-697-1

Query Match 19.4%; Score 39.5; DB 3; Length 27;
Best Local Similarity 58.3%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 7 GKCHCHMGTHCH 18
Db 1 GSC-CHTGNHHD 11

RESULT 9
US-08-466-248-1
; Sequence 1, Application US/08466248
; Patent No. 6258359
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauerbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thiberge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,248
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,177
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,697

; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0137-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-248-1

Query Match 19.4%; Score 39.5; DB 3; Length 27;
Best Local Similarity 58.3%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHCH 18
DB 1 GSC-CHTGNHGH 11

RESULT 10
US-09-894-882-471
; Sequence 471, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 471
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus figulinus
US-09-894-882-471

Query Match 19.4%; Score 39.5; DB 4; Length 30;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 9 CHCHMGTHCHSSDGRGV 26
DB 1 CH-HEGLPCTSDGCCGM 17

RESULT 11
US-09-894-882-474
; Sequence 474, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 474
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus figulinus
US-09-894-882-474

Query Match 19.4%; Score 39.5; DB 4; Length 30;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 9 CHCHMGTHCHSSDGRGV 26
DB 1 CH-HEGLPCTSDGCCGM 17

RESULT 12
US-09-894-882-475
; Sequence 475, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14

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SOFTWARE: Patentin release #1.0, Version #1.1.2
CURRENT APPLICATION DATA:
  FILING DATE:
  APPLICATION NUMBER: US/08/486.013
  CLASSIFICATION: 530
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/342,268
    FILING DATE: 18-NOV-1994
    APPLICATION NUMBER: US 07/930,649
    FILING DATE: 14-AUG-1992
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/889,020
      FILING DATE: 26-MAY-1992
      ATTORNEY/AGENT INFORMATION:
        NAME: Campbell, Cathryn A.
        REGISTRATION NUMBER: 31,815
        REFERENCE/DOCKET NUMBER: P-UC 1206
        TELECOMMUNICATION INFORMATION:
          TELEPHONE: (619) 535-9001
          TELEFAX: (619) 535-8949
          INFORMATION FOR SEQ ID NO: 9:
            SEQUENCE CHARACTERISTICS:
              LENGTH: 31 amino acids

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:17:52 ; Search time 37 Seconds
(without alignments)
39,007 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPPERTLEGSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	30.6	15	2 A60763	endo-1,3-beta-gluc
2	24	28.2	13	2 G61458	ig lambda chain V-
3	22.5	26.5	12	2 FS0213	28K protein 4412 -
4	22	25.9	10	2 C35369	urease (EC 3.5.1.5
5	22	25.9	11	2 S13279	ile-Ser-bradykinin
6	21	24.7	11	2 I33098	173K exantigen -
7	21	24.7	13	1 XAV19B	angiotensin-conver
8	21	24.7	15	2 B39109	hypothetical 1.5K
9	20	23.5	9	2 S19229	sperm-activating p
10	20	23.5	12	2 S43013	hypothetical prote
11	20	23.5	12	2 FN0046	ATP synthase D cha
12	20	23.5	12	2 PD0021	muconate cyclisom
13	20	23.5	14	2 PH1705	ig heavy chain V r
14	20	23.5	15	2 PX0031	mixed lymphocyte i
15	19	22.4	7	2 S71239	IC12 protein - Par
16	19	22.4	7	2 FT0283	ig heavy chain CRD
17	19	22.4	9	2 PT0231	ig heavy chain CDR
18	19	22.4	10	2 D61440	polygalacturonase
19	19	22.4	11	2 S21127	precorrin methyltr
20	19	22.4	11	2 YHHU	morphogenetic neur
21	19	22.4	11	2 YHBO	morphogenetic neur
22	19	22.4	11	2 YHJFYH	morphogenetic neur
23	19	22.4	11	2 YHAE	morphogenetic neur
24	19	22.4	11	2 YHRT	morphogenetic neur
25	19	22.4	12	2 PN0663	dystrophin-associa
26	19	22.4	12	2 I58273	thyroglobulin - ra
27	19	22.4	13	2 D39690	neural cell adhesi
28	19	22.4	14	2 C40944	hypothetical prote
29	19	22.4	14	2 S19803	ubiquitin - potato

30 19 22.4 14 2 H64008 hypothetical prote
31 19 22.4 14 2 S65392 cytochrome-c oxida
32 19 22.4 14 2 A17150 glucose 1-dehydrog
33 19 22.4 15 2 PQ0232 cystatin Cl-4a - m
34 19 22.4 15 2 PA0014 seed storage prote
35 19 22.4 15 2 PN0173 flt3 ligand isofor
36 19 22.4 15 2 I78838 ubiquitin - fungus
37 19 22.4 15 2 PA0063 apolipoprotein A-I
38 19 22.4 15 2 A60221 Ig heavy chain CRD
39 18 21.2 10 2 PT0289 spermadhesin AQN-3
40 18 21.2 11 2 S68649 sterol carrier pro
41 18 21.2 12 2 A61503 frame shifted cyta
42 18 21.2 12 4 S49073 T-cell-specific tr
43 18 21.2 13 2 S61798 histone H4-1 precu
44 18 21.2 14 2 IS1432 probursin tetradec
45 18 21.2 14 2 JH0328

ALIGNMENTS

RESULT 1

A60763
endo-1,3-beta-glucanase (EC 3.2.1.-), 68k - Bacillus circulans (strain WL-12) (fragment
C:Species: Bacillus circulans
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C:Accession: A60763
R: Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.
J. Gen. Microbiol. 136, 2377-2383, 1990
A:Title: Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-beta-gluc
A:Reference number: A60763; MUID:91178514; PMID:2127800
A:Accession: A60763
A:Molecule type: protein
A:Residues: 1-15 <PIS>
C:Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth on
C:Keywords: glycosidase; hydrolase

Query Match 30.6%; Score 26; DB 2; Length 15;

Best Local Similarity 40.0%; Pred. No. 6.2e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 PBIRTEGSC 15

|||:|:|

DB 3 PEVTSMEYFC 12

RESULT 2

G61458
IG lambda chain V-II region (AZI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: G61458; F00159
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idioctype by human monoclonal IgM directed to myelin-ass
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: G61458
A:Molecule type: Protein
A:Residues: 1-13 <BKO>
C:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycop
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.2%; Score 24; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 1.2e+03;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSQPPET 8

:|:|:|:

DB 4 LTQPPSV 10

RESULT 3

FS0213

28K protein 4412 - rice (strain Nihonbare) (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: PS0213
 R:Tsugita, A.; Kamo, M.
 submitted to JIPID, April 1993
 A:Reference number: PS0209
 A:Accession: PS0213
 A:Molecule type: protein
 A:Residues: 1-12 <TSU>
 A:Cross-references: UNIPROT:Q7M280
 A:Experimental source: callus
 C:Comment: molecular weight 28K, pI 4.6.

Query Match 26.5%; Score 22.5; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 5 PPEIR-TLEG 13
 ||||
 DB 3 PPEFTGTTEG 12

RESULT 4

C35389
 urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
 C:Species: Morganella morganii
 C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
 C:Accession: C35389
 R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
 J. Bacteriol. 172, 3073-3080, 1990
 A:Title: Morganella morganii urease: purification, characterization, and isolation of gene
 A:Reference number: A35389; MUID:90264298; PMID:2345135
 A:Accession: C35389
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <HUA>
 A:Cross-references: UNIPROT:P17339
 C:Keywords: hydrolase

Query Match 25.9%; Score 22; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPEI 8
 ||||
 DB 5 PPEV 8

RESULT 5

S13279
 Ile-Ser-bradykinin - human (fragment)
 N:Alternate names: T-kinin
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S13279
 R:Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.
 Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
 A:Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignan
 A:Reference number: S13279; MUID:91166748; PMID:2076202
 A:Accession: S13279
 A:Molecule type: protein
 A:Residues: 1-11 <WUN>
 A:Cross-references: UNIPROT:Q7M4P1
 C:Keywords: bradykinin

Query Match 25.9%; Score 22; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSQPP 6
 :|||
 DB 1 ISRPP 5

RESULT 6

I33098
 173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: I33098
 R:Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: I33098
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <NIC>

Query Match 24.7%; Score 21; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPEI 8
 ||||
 DB 3 PPEL 6

RESULT 7

XAVI9B
 angiotensin-converting enzyme inhibitor V-9 - jararaca
 C:Species: Bothrops jararaca (jararaca)
 C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
 C:Accession: A01253
 R:Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocoy, O.
 Biochemistry 10, 4033-4039, 1971
 A:Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. I
 A:Reference number: A90356; MUID:72118526; PMID:4334402
 A:Accession: A01253
 A:Molecule type: protein
 A:Residues: 1-13 <OND>
 A:Cross-references: UNIPROT:P01020
 A:Note: the structure of the peptide was confirmed by synthesis
 C:Comment: This peptide also potentiates bradykinin by inhibiting the kinases that inact
 C:Superfamily: bradykinin-potentiating peptide
 C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
 F.1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 24.7%; Score 21; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVSQPPPEI 8
 ||||
 DB 4 WPRPGPEI 11

RESULT 8

B39109
 hypothetical 1.5K protein - hepatitis C virus
 N:Alternate names: hypothetical protein 2
 C:Species: hepatitis C virus
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
 C:Accession: B39109; J01585
 R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
 A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identificati
 A:Reference number: A39109; MUID:91156678; PMID:1705704
 A:Accession: B39109
 A>Status: not compared with conceptual translation
 A:Molecule type: rRNA
 A:Residues: 1-15 <HAN>
 A:Cross-references: GB:M58406
 R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A:Title: Cloning and sequencing of the structural region and expression of putative core

A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: JQ1584; MUID:92300349; PMID:1318944
A:Accession: JQ1585
A:Molecule type: genomic RNA
A:Residues: 1-15 <KUM>
A:Experimental source: strain U.K.

Query Match 24.7%; Score 21; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSOPP 6
|
|
|
|
DB 3 VQOPP 7

RESULT 9

S19329
sperm-activating peptide SAP - sea urchin (Stomopneustes variolus)
C:Species: Stomopneustes variolus
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 16-Aug-2004
C:Accession: S19329
R:Yoshino, K.; Takao, T.; Shimonishi, Y.; Suzuki, N.
FEBS Lett. 294, 179-182, 1991
A:Title: Determination of the amino acid sequence of an intramolecular disulfide linkage
A:Reference number: S19329; MUID:92097763; PMID:1756858
A:Accession: S19329
A:Molecule type: protein
A:Residues: 1-9 <YOS>
F:3-8/Disulfide bonds: #status predicted

Query Match 23.5%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 EGSC 15
|
|
|
|
DB 5 EGKC 8

RESULT 10

S43013
hypothetical protein URF-2X - Yersinia enterocolitica transposon TN3926
C:Species: Yersinia enterocolitica
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43013
R:Osbourne, S.E.V.; Turner, A.K.; Grinstead, J.
submitted to the EMBL Data Library, March 1994
A:Description: The structure of the bacterial transposable element, TN3926.
A:Reference number: S43011
A:Accession: S43013
A:Molecule type: DNA
A:Residues: 1-12 <OSB>
A:Cross-references: UNIPROT:Q52112; EMBL:X78059; NID:g460067; PIDN:CAA54979.1; PID:g4600
C:Genetics:
A:Mobile element: transposon TN3926

Query Match 23.5%; Score 20; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQPPE 7
|
|
|
|
DB 4 SQPAE 8

RESULT 11

PN0046
ATP synthase D chain, mitochondrial - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 09-Jul-2004
C:Accession: PN0046
R:Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996

A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: PN0041
A:Accession: PN0046
A:Molecule type: protein
A:Residues: 1-12 <KAT>
A:Cross-references: UNIPROT:Q9DCX2
A:Experimental source: neuroblastoma cell
C:Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blocked.
C:Keywords: brain; mitochondrion

Query Match 23.5%; Score 20; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVSQP 5
|
|
|
|
DB 4 WPHQP 8

RESULT 12

PN0021
muconate cycloisomerase (EC 5.5.1.1) II - Frateuria sp. ANA-18 (fragment)
N:Alternate names: MC II
C:Species: Frateuria sp. ANA-18
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: PD0021
R:Murakami, S.; Takemoto, J.; Takashima, A.; Shinke, R.; Aoki, K.
Biosci. Biotechnol. Biochem. 62, 1129-1133, 1998
A:Title: Purification and characterization of two muconate cycloisomerase isozymes from
A:Reference number: PD0020; MUID:98357223; PMID:9692194
A:Accession: PD0021
A:Molecule type: protein
A:Residues: 1-12 <MUR>
A:Cross-references: UNIPROT:Q929Y1
C:Keywords: intramolecular lyase; isomerase

Query Match 23.5%; Score 20; DB 2; Length 12;
Best Local Similarity 27.3%; Pred. No. 4.9e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSQPPEIRTE 12
|
|
|
|
DB 2 IATPVKIESVE 12

RESULT 13

PH1705
Ig heavy chain V region (clone ASC-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1705
R:McHeyzar-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1705
A:Molecule type: mRNA
A:Residues: 1-14 <MCH>
A:Experimental source: B cell
A>Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 12
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.5%; Score 20; DB 2; Length 14;
Best Local Similarity 30.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WVSQPPEIRT 10
|
|
|
|
DB 4 WVRNTKSVET 13

RESULT 14

PX0031
 mixed lymphocyte reaction inhibitor - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C;Accession: PX0031
 R;Shinomiya, T.; Ohara, T.; Wada, N.; Omori, A.; Kamada, N.
 J. Biochem. 107, 435-439, 1990
 A;Title: Rat liver arginase suppresses mixed lymphocyte reaction.
 A;Reference number: PX0031; MUID:90256720; PMID:2140355
 A;Accession: PX0031
 A;Molecule type: protein
 A;Residues: 1-15 <SHI>
 A;Cross-references: UNIPROT:Q7M040
 A;Experimental source: liver
 C;Keywords: lymphocyte

Query Match 23.5%; Score 20; DB 2; Length 15;
 Best Local Similarity 25.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WVSQPPETILE 12
 | : : : :
 Db 4 WMSMSKPKPIE 15

RESULT 15
 S71299
 ICL2 protein - Paramecium tetraurelia (fragment)
 C;Species: Paramecium tetraurelia
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C;Accession: S71299
 R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A;Title: Characterization of centrin genes in Paramecium.
 A;Reference number: S71298; MUID:96248429; PMID:8665928
 A;Accession: S71299
 A;Molecule type: protein
 A;Residues: 1-7 <MAD>
 A;Experimental source: strain d4-2
 C;Genetics:
 A;Genetic code: SGC5

Query Match 22.4%; Score 19; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QPP 6
 | : : :
 Db 2 QPP 4

Search completed: November 16, 2004, 19:48:22
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:38:57 ; Search time 189 Seconds
(without alignments)
45.665 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85
Sequence: 1 WVSQPFIRTLGSC 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	28.2	11	2 Q80W11	Q80W11 mus sp. nt-
2	24	28.2	11	2 Q9L8K1	Q9L8K1 enterococcu
3	24	28.2	15	2 Q95773	Q95773 conolophus
4	23	27.1	11	2 Q70056	Q70056 mycoplasma
5	23	27.1	11	2 CAF32692	CAF32692 mycoplasma
6	23	27.1	11	2 CAF32694	CAF32694 mycoplasma
7	23	27.1	11	2 CAF32696	CAF32696 mycoplasma
8	23	27.1	13	2 Q9UDC6	Q9UDC6 homo sapien
9	23	27.1	13	2 Q7BS48	Q7BS48 streptomyce
10	22.5	26.5	12	2 Q7M280	Q7M280 oryza sativ
11	22	25.9	9	2 P82429	P82429 nicotiana t
12	22	25.9	10	1 URE3_MORMO	URE3_MORMO
13	22	25.9	11	2 Q16217	Q16217 morganella
14	22	25.9	11	2 Q7M4P1	Q7M4P1 homo sapien
15	22	25.9	12	2 Q9B249	Q9B249 homo sapien
16	22	25.9	13	2 Q43174	Q43174 solanum tub
17	22	25.9	14	2 Q26075	Q26075 psammehinu
18	21	24.7	8	2 Q8W8G3	Q8W8G3 diadema sav
19	21	24.7	8	2 Q8W8G4	Q8W8G4 diadema pau
20	21	24.7	8	2 Q8W8G5	Q8W8G5 diadema mex
21	21	24.7	9	2 Q8W8W5	Q8W8W5 diadema ant
22	21	24.7	9	2 Q8W8W6	Q8W8W6 diadema ant
23	21	24.7	9	2 Q8W8X4	Q8W8X4 diadema mex
24	21	24.7	10	2 Q8WFS4	Q8WFS4 diadema mex
25	21	24.7	10	2 Q8WFT5	Q8WFT5 diadema ant
26	21	24.7	13	1 BPPI_BOTJA	BPPI_BOTJA
27	21	24.7	13	1 EP65_HUMAN	EP65_HUMAN
28	21	24.7	13	1 Q85C99	Q85C99 homo sapien
29	21	24.7	14	2 Q85CA0	Q85CA0 strongyloce
30	21	24.7	14	2 Q85CA1	Q85CA1 strongyloce
31	21	24.7	14	2 Q85CA2	Q85CA2 strongyloce

32	21	24.7	14	2 Q85CA2	Q85CA2 strongyloce
33	21	24.7	14	2 Q85I00	Q85I00 strongyloce
34	21	24.7	14	2 Q85I03	Q85I03 pseudocentr
35	21	24.7	14	2 Q85I10	Q85I10 strongyloce
36	21	24.7	14	2 Q85I14	Q85I14 strongyloce
37	21	24.7	14	2 Q85I17	Q85I17 hemacentrot
38	21	24.7	14	2 Q85I20	Q85I20 strongyloce
39	21	24.7	14	2 Q85I26	Q85I26 allocentrot
40	21	24.7	15	2 Q9S8N8	Q9S8N8 hordeum vul
41	20	23.5	7	2 P92210	P92210 agropyron c
42	20	23.5	7	2 P92214	P92214 amblyopyrum
43	20	23.5	7	2 P92218	P92218 australopyr
44	20	23.5	7	2 P92221	P92221 bromus iner
45	20	23.5	7	2 P92226	P92226 crithopeis

ALIGNMENTS

RESULT 1
ID Q80W11 PRELIMINARY; PRT; 11 AA.
AC Q80W11;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE NT-3 transcript A (Fragment).
GN Name=NT-3;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95040015; PubMed=7952296;
RT Leingartner A., Lindholm D.;
RT "Two promoters direct transcription of the mouse NT-3 gene.";
RL Eur. J. Neurosci. 6:1149-1159(1994).
DR EMBL; S75812; AAP31855.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1348 MW; 2280047D0DC5A777 CRC64;

Query Match 28.2%; Score 24; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 QPPEIRTL 11
DB 3 QPPSARIM 10

RESULT 2
ID Q9L8K1 PRELIMINARY; PRT; 13 AA.
AC Q9L8K1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Vans (Fragment).
GN Name=vans;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EM4281;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to Tn382 in vancomycin
resistant enterococci and characterization of two novel insertion
sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF201896; AAF73374.1; -.

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FT  NON TER      1      1
SQ  SEQUENCE    13 AA; 1502 MW;  8D0E282189F9672A CRC64;

Query Match
Best Local Similarity  28.2%; Score 24; DB 2; Length 13;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 WVSQPP 6
   |: ||
Db  4 WLDLPP 9

RESULT 3
Q95773 PRELIMINARY; PRT; 15 AA.
AC Q95773;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN Name=ND4;
OS Coriophorus subriatus (Galapagos land iguana).
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Conolophus.
OX NCBI_TaxID=31140;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=97019047; PubMed=885663;
RA Sites J.W., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RT "Character congruence and phylogenetic signal in molecular and
RT morphological data sets: a case study in the living Iguanas (Squamata,
RT Iguanidae)";
RL Mol. Biol. Evol. 13:1087-1105 (1996).
RN [2];
RP SEQUENCE FROM N.A.
RA Sites J.W., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U66235; AAB07475.1; -.
DR GO; GO:0005739; C.mitochondrion; IEA.
KW Mitochondrion.
FT  NON TER      1      1
SQ  SEQUENCE    15 AA; 1839 MW;  9263179CE68523B1 CRC64;

Query Match
Best Local Similarity  28.2%; Score 24; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  9 RTLEGSC 15
   |: ||
Db  3 RRLHGTC 9

RESULT 4
Q700S6 PRELIMINARY; PRT; 11 AA.
AC Q700S6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Variable adherence associated protein (Fragment).
GN Name=vaa;
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=type strain: PG21;
RA Boesen T.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ629114; CAF32694.1; -.
DR EMBL; AJ629115; CAF32696.1; -.
DR EMBL; AJ629113; CAF32692.1; -.

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FT  NON TER      1      1
SQ  SEQUENCE    11 AA; 1376 MW;  C22D517B5B133736 CRC64;

Query Match
Best Local Similarity  27.1%; Score 23; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 WVSQPPERT 10
   |: ||
Db  1 WKDQLKEIST 10

RESULT 5
CAF32692 PRELIMINARY; PRT; 11 AA.
ID CAF32692;
AC CAF32692;
DT 31-MAR-2004 (TrEMBLrel. 27, Created)
DT 31-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 31-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Variable adherence associated protein (Fragment).
GN VAA.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=4195;
RA Boesen T.;
RL "Gene and protein structure of the Mycoplasma hominis vaa adhesin.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ629113; CAF32692.1; -.
FT  NON TER      1      1
SQ  SEQUENCE    11 AA; 1376 MW;  C22D517B5B133736 CRC64;

Query Match
Best Local Similarity  27.1%; Score 23; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 WVSQPPERT 10
   |: ||
Db  1 WKDQLKEIST 10

RESULT 6
CAF32694 PRELIMINARY; PRT; 11 AA.
ID CAF32694;
AC CAF32694;
DT 31-MAR-2004 (TrEMBLrel. 27, Created)
DT 31-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 31-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Variable adherence associated protein (Fragment).
GN VAA.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=type strain: PG21;
RA Boesen T.;
RL "Gene and protein structure of the Mycoplasma hominis vaa adhesin.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ629114; CAF32694.1; -.
FT  NON TER      1      1
SQ  SEQUENCE    11 AA; 1376 MW;  C22D517B5B133736 CRC64;

Query Match
Best Local Similarity  27.1%; Score 23; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 WVSQPPERT 10
   |: ||
Db  1 WKDQLKEIST 10

RESULT 7
CAF32694 PRELIMINARY; PRT; 11 AA.
ID CAF32694;
AC CAF32694;
DT 31-MAR-2004 (TrEMBLrel. 27, Created)
DT 31-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 31-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Variable adherence associated protein (Fragment).
GN VAA.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=type strain: PG21;
RA Boesen T.;
RL "Gene and protein structure of the Mycoplasma hominis vaa adhesin.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ629114; CAF32694.1; -.
FT  NON TER      1      1
SQ  SEQUENCE    11 AA; 1376 MW;  C22D517B5B133736 CRC64;

Query Match
Best Local Similarity  27.1%; Score 23; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 WVSQPPERT 10
   |: ||
Db  1 WKDQLKEIST 10

```



```

GN Name=hrdb;
OS Streptomyces aureofaciens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCM 3239;
RA MEDLINE=99132018; PubMed=9931449;
RX Kormanec J., Novakova R., Homerova D., Sevcikova B.;
RT "The Streptomyces aureofaciens homologue of the sporulation gene whiH
is dependent on rpoZ-encoded sigma factor.";
RL Biochim. Biophys. Acta 1444:80-84(1999).
DE EMBL: AF096293; AAD09768.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1390 MW; 8F198834E708B415 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPEI 8
DB 10 PPEI 13

RESULT 10
Q7M280 PRELIMINARY; PRT; 12 AA.
ID Q7M280;
AC Q7M280;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 28K protein 4412 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Tsugita A., Kamo M.;
RL Submitted (APR-1993) to the PIR data bank.
DR PIR; PS0213; PS0213.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1163 MW; 6C2E467AAD61A9CB CRC64;

Query Match 26.5%; Score 22.5; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 9.5e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 5 PPEIR-TLEG 13
DB 3 PPEITGITEG 12

RESULT 11
P82429 PRELIMINARY; PRT; 9 AA.
ID P82429;
AC P82429;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 24, Last annotation update)
DE 44 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;

Query Match 27.1%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.1e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVSQPPEIRT 10
DB 1 WKDQLKEIST 10

RESULT 8
Q9UDC6 PRELIMINARY; PRT; 13 AA.
ID Q9UDC6;
AC Q9UDC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ENDOTHELUM-derived RELATING factor, nitric oxide synthase
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054573; PubMed=1385404;
RA Janssens S.P., Simouchi A., Quettermous T., Bloch D.B., Bloch K.D.;
RT "Cloning and expression of a cDNA encoding human endothelium-derived
relating factor/nitric oxide synthase.";
RL J. Biol. Chem. 267:22694-22694(1992).
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7EB867 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVSQPP 6
DB 1 WAFDPP 6

RESULT 9
Q7BS48 PRELIMINARY; PRT; 13 AA.
ID Q7BS48;
AC Q7BS48;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Sigma factor (Fragment).

```

```

GN Name=hrdb;
OS Streptomyces aureofaciens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCM 3239;
RA MEDLINE=99132018; PubMed=9931449;
RX Kormanec J., Novakova R., Homerova D., Sevcikova B.;
RT "The Streptomyces aureofaciens homologue of the sporulation gene whiH
is dependent on rpoZ-encoded sigma factor.";
RL Biochim. Biophys. Acta 1444:80-84(1999).
DE EMBL: AF096293; AAD09768.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1390 MW; 8F198834E708B415 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPEI 8
DB 10 PPEI 13

RESULT 10
Q7M280 PRELIMINARY; PRT; 12 AA.
ID Q7M280;
AC Q7M280;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 28K protein 4412 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Tsugita A., Kamo M.;
RL Submitted (APR-1993) to the PIR data bank.
DR PIR; PS0213; PS0213.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1163 MW; 6C2E467AAD61A9CB CRC64;

Query Match 26.5%; Score 22.5; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 9.5e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 5 PPEIR-TLEG 13
DB 3 PPEITGITEG 12

RESULT 11
P82429 PRELIMINARY; PRT; 9 AA.
ID P82429;
AC P82429;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 24, Last annotation update)
DE 44 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;

```

RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Siabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO: GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON TER
SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C77776 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SOPPE 7
:|:|:
Db 1 AQPPO 5

RESULT 12

URE3 MORMO
ID URE3 MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)
DE (Urease 6 kDa subunit) (Fragment).
GN Name:ureh;
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii ureases: purification, characterization, and
RT isolation of gene sequences";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the urease gamma subunit family.
DR PIR; C35389; C35389.
DR HAMAP; MF_00739; -; 1.
KW Direct protein sequencing; Hydrolase.
FT NON TER
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 25.9%; Score 22; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPEI 8
:|:|:
Db 5 PPEV 8

RESULT 13

Q16217
ID Q16217 PRELIMINARY; PRT; 11 AA.
AC Q16217; (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE Argininosuccinate synthetase protein (Fragment).
GN Name=argininosuccinate synthetase;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95067972; PubMed=7977368;
RA Kobayashi K., Shaheen N., Terazono H., Saeki T.;
RT "Mutations in argininosuccinate synthetase mRNA of Japanese patients,
RT causing classical citrullinemia";
RL Am. J. Hum. Genet. 55:1103-1112(1994).
DR EMBL; S73202; AAD14115.1; -;
FT NON TER
SQ SEQUENCE 11 AA; 1024 MW; 3DD920EC6B058728 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSQPEI 8
:|:|:|:
Db 5 LSEPPGV 11

RESULT 14

Q7M4P1
ID Q7M4P1 PRELIMINARY; PRT; 11 AA.
AC Q7M4P1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ile-Ser-bradykinin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=91166748; PubMed=2076202;
RA Wunderer G., Walter I., Eschenbacher B., Lang M., Kellermann J.,
RA Kindermann G.;
RT "Ile-Ser-bradykinin is an aberrant permeability factor in various
RT human malignant effusions";
RL Biol. Chem. Hoppe-Seyler 371:977-981(1990).
DR PIR; S13279; S13279.
FT NON TER
FT NON TER
SQ SEQUENCE 11 AA; 1260 MW; 33D55258B9C86777 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSQPP 6
:|:|:
Db 1 ISRPP 5

RESULT 15

Q9B249
ID Q9B249 PRELIMINARY; PRT; 12 AA.
AC Q9B249;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Glycophorin C (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
RA Zimmerman P.A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342984; AAK01459.1; -.

FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. NO. 1.2e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVSQPPE 7
Db 6 WPLPPQ 12

Search completed: November 16, 2004, 19:51:37
Job time : 190 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:16:07 ; Search time 150 Seconds
(without alignments)
35.873 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPEIRTLGSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	85	100.0	15	4 AAE02774	Aae02774 Human Nkp
2	85	100.0	15	8 ADQ30927	Adq30927 Human Nkp
3	35	41.2	13	2 AA04804	Aa04804 Human Glu
4	35	41.2	14	2 AAR76661	Aar76661 Peptide d
5	35	41.2	14	2 AA018869	Aa018869 65 KD Glu
6	35	41.2	15	2 AA012410	Aa012410 GAD65 res
7	34	40.0	12	7 ADC88750	Adc88750 Payers pa
8	34	40.0	12	7 ADC22832	Adc22832 Intestina
9	34	40.0	15	8 ADG17041	Adg17041 Human imm
10	33	38.8	9	5 ABG67474	Abg67474 Human ADP
11	33	38.8	9	6 ADA23585	Ada23585 Alzheimer
12	33	38.8	14	2 AAR37328	Aar37328 Humanised
13	33	38.8	14	5 AAU70479	Aau70479 Mouse hea
14	33	38.8	14	5 AAU70495	Aau70495 Mouse hea
15	33	38.8	14	6 AB018543	Ab018543 Ganglios
16	33	38.8	14	6 ABO10781	Ab010781 Murine E9
17	33	38.8	14	6 ABR44725	Ab44725 Murine E9
18	33	38.8	14	7 ADI25283	Adi25283 NEWM heav
19	33	38.8	14	7 ADM07637	Adm07637 Canine im
20	33	38.8	14	7 ADM07564	Adm07564 Canine im
21	33	38.8	14	7 ADM07638	Adm07638 Canine im
22	33	38.8	14	7 ADM07560	Adm07560 Canine im
23	33	38.8	14	8 ADF94447	Adf94447 Humanised
24	33	38.8	15	8 ADG17029	Adg17029 Human imm
25	32	37.6	9	8 ADK02306	Adk02306 Hepatitis

26	32	37.6	9	8 ADK02317	Adk02317 Hepatitis
27	32	37.6	10	7 ADC22900	Adc22900 Beta case
28	32	37.6	13	2 AAW00509	Aaw00509 Human gro
29	32	37.6	13	7 ADC61255	Adc61255 Human hGH
30	32	37.6	13	7 ADC61276	Adc61276 Human hGH
31	32	37.6	14	2 AAR77216	Aar77216 Mouse ant
32	32	37.6	14	2 AAR70461	Aar70461 VH sequen
33	32	37.6	14	2 AAR87054	Aar87054 Rat MAb 3
34	32	37.6	14	3 AAY56293	Aay56293 FR2 gener
35	32	37.6	14	5 AAU70507	Aau70507 Mouse hea
36	32	37.6	14	5 AAU70467	Aau70467 Human hea
37	32	37.6	15	2 AAY01512	Aay01512 Human gro
38	32	37.6	15	2 AA002650	Aa002650 Human gro
39	32	37.6	15	2 AAY01667	Aay01667 Peptide a
40	32	37.6	15	2 AAY01681	Aay01681 Peptide a
41	32	37.6	15	2 AAY01678	Aay01678 Peptide a
42	32	37.6	15	2 AAY01653	Aay01653 Peptide a
43	32	37.6	15	2 AAY01660	Aay01660 Peptide a
44	32	37.6	15	2 AAY01668	Aay01668 Peptide a
45	32	37.6	15	2 AAY01679	Aay01679 Peptide a

ALIGNMENTS

RESULT 1

AAE02774

ID AAE02774 standard; peptide; 15 AA.

XX AC AAE02774;

XX AC AAE02774;

DT 06-AUG-2001 (first entry)

DE Human Nkp30 receptor immunogenic peptide for antiserum production.

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;

KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;

KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;

KW therapy.

XX Homo sapiens.

XX WO200136630-A2.

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000MO-EP011697.

XX PR 15-NOV-1999; 99CA-02288307.

XX PR 15-NOV-1999; 99US-00440514.

XX PA (INNA-) INNATE PHARMA SAS.

XX PA (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

XX Novel compound, useful for detection and/or quantifying the presence of

PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.

PT Claim 1; Page 33; 83pp; English.

XX The invention relates to human Nkp30 receptor and its corresponding cDNA

CC molecule which is involved in natural cytotoxicity mediated by natural

CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor

CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively

CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are

CC useful for detecting and/or quantifying the presence of NK cells in a

CC biological sample. The invention also provide kits for detecting and/or

CC quantifying the presence of NK cells, for the selective removal of NK

CC cells from a biological sample, for the positive and selective

CC purification of NK cells from a biological sample and for the in vitro

CC stimulation of NK cell cytotoxicity. The invention further provides a
 CC pharmaceutical composition which is used as a drug for grafting
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft
 CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for
 CC the prevention, palliation and/or therapy of solid or liquid tumours,
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
 CC microorganism, notably viral infection. NKp30 antibodies are useful for
 CC identifying NKp30 natural ligands and allow assessment of the level of
 CC surface NKp30 ligand expressed on an NK-susceptible target cell and the
 CC comparison of this level to the standard physiological one. Hence NKp30
 CC antibodies are useful in the diagnosis of tumours or of infection. The
 CC present sequence is human NKp30 receptor immunogenic peptide fragment
 CC which is used for NKp30 polyclonal antiserum production
 XX
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 85; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WVSQPPPIRTLEGSC 15
 DB 1 WVSQPPPIRTLEGSC 15
 RESULT 2
 ADQ30927
 ID ADQ30927 standard; peptide; 15 AA.
 XX
 AC ADQ30927;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human NKp30 immunogenic peptide.
 XX
 DE Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial;
 KW immunogen.
 KW
 KW Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 15
 FT /note= "Non-native C-terminal Cys residue"
 XX
 XX W02004056392-A1.
 XX
 PD 08-JUL-2004.
 XX
 XX 22-DEC-2003; 2003WO-EP014716.
 XX
 XX 23-DEC-2002; 2002US-0435344P.
 XX
 XX (INNA-) INNATE PHARMA.
 XX
 XX Romagne F, Andre P;
 XX
 XX WPI; 2004-507595/48.
 XX
 XX Pharmaceutical compositions that stimulate proliferation of natural
 PT killer cells useful for therapy of melanoma, chronic myeloid, and
 PT leukemia, comprise an anti-natural killer cell receptor antibody and
 PT interleukins.
 XX
 XX Claim 3; SEQ ID NO 5; 35pp; English.
 XX
 XX The present sequence is that of an immunogenic peptide derived from human
 CC NKp30 ADQ30923, a 190 amino acid polypeptide that is selectively
 CC expressed by natural killer (NK) cells, and particularly by mature NK
 CC cells. Claimed pharmaceutical compositions that have a stimulating effect
 CC on the proliferation of NK cells comprise an antibody such as an anti-
 CC NKp30 antibody or anti-NKp46 antibody or its immuno-reactive fragment and
 CC a cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the

CC antibody(ies) and cytokine(s) being administered together or separately
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its
 CC antigen-binding fragment which specifically binds to NKp30 or to a
 CC fragment, including the present immunogenic peptide, of NKp30. The
 CC pharmaceutical compositions, when used for daily subcutaneous injection,
 CC comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and
 CC lower than 1 million units/square meters/day of cytokine(s), are useful
 CC for the prevention, palliation and therapy of e.g. melanoma, chronic
 CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
 CC prevention, palliation and therapy (claimed).
 XX
 XX Sequence 15 AA;
 Query Match 100.0%; Score 85; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WVSQPPPIRTLEGSC 15
 DB 1 WVSQPPPIRTLEGSC 15
 RESULT 3
 AAW04804
 ID AAW04804 standard; peptide; 13 AA.
 XX
 AC AAW04804;
 XX
 DT 29-APR-1997 (first entry)
 XX
 DE Human glutamic acid decarboxylase peptide amino acids 506-518.
 XX
 XX Human; pro-insulin; T cell; insulin dependent diabetes mellitus; IDDM;
 KW function; glutamic acid decarboxylase; assay; auto-antibody; adsorbent.
 KW
 XX Homo sapiens.
 OS
 XX WO9626218-A1.
 XX
 XX 29-AUG-1996.
 PD
 XX 20-FEB-1996; 96WO-AU000085.
 PF
 XX 20-FEB-1995; 95AU-00001239.
 PR
 XX 04-SEP-1995; 95AU-00005172.
 PR
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA
 XX Harrison L, Honeyman M, Rudy G, Lew A;
 XX
 XX WPI; 1996-402321/40.
 XX
 XX Human glutamic acid decarboxylase 65 or pro-insulin epitopic peptide(s) -
 PT modify T cell function in cells from insulin dependent diabetes mellitus
 PT (IDDM) patients, useful for assaying reactivity to IDDM auto-antigen.
 XX
 XX Claim 6; Page 23; 36pp; English.
 PS
 XX This peptide sequence represents amino acids 506-518 of human glutamic
 CC acid decarboxylase which is used in a novel peptide which reacts with and
 CC modifies the function of T cells from patients with (pre-)clinical
 CC insulin dependent diabetes mellitus (IDDM). The peptide forms the central
 CC section of the novel peptide of formula: X1-X2-X3, where X1 and X3 are,
 CC independently, 0-40 amino acids (natural or synthetic). Alternatively,
 CC the central section (X2) may be homologous or contiguous with the amino
 CC acid sequence corresponding to amino acids 24-36 of human pro-insulin
 CC (AAW04803). The novel peptides are used in claimed methods for assaying
 CC reactivity of a subject to IDDM autoantibodies. Also the peptides can be
 CC used to treat diabetes by acting as an adsorbent for IDDM autoantibodies
 XX
 XX Sequence 13 AA;

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Query Match      41.2%; Score 35; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 PPEIRTLTLE 12
   ||:|||||
Db 5 PPSLRITLLE 12

RESULT 4
AAW76661
ID AAR76661 standard; peptide; 14 AA.
XX
AC AAR76661;
XX
DT 05-MAR-1996 (first entry)
XX
DE Peptide derived from human glutamic acid decarboxylase 20.
KW diabetes; T-cell subpopulation; detection; antigen production; diagnosis;
KW autoimmune disease.
XX
OS Homo sapiens.
XX
PN DB4418091-A1.
XX
PD 27-JUL-1995.
XX
PF 24-MAY-1994; 94DE-04418091.
XX
PR 20-JAN-1994; 94DE-04401629.
PR 04-FEB-1994; 94DE-04403522.
XX
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI Endl J, Stahl P, Albert W, Jung G, Schendel D, Meinl E;
PI Dormmair K;
XX
DR WPI; 1995-264505/35.
XX
PT Antigen-specific activated T-lymphocytes and their detection - by
PT interaction with inventive peptide(s) of peptide-MHC complexes; useful in
PT diagnosis of e.g. diabetes and autoimmune diseases.
XX
PS Claim 1; Fig 2; 21pp; German.
XX
CC AAR76642-62 are derived from human glutamic acid decarboxylase and
CC specifically react with T-cell sub-populations isolated from recently
CC diagnosed Type-1 diabetics. Pharmaceutical compans. contg. these peptides
CC and those shown in AAR77571-72, are useful for the diagnosis of a disease
CC or predispositions of immune system diseases, tumours, and autoimmune
CC diseases, including diabetes. The peptides are able to detect specific T-
CC cell subpopulations that are then used for antigen prodn., e.g. by
CC reinjection
XX
SQ Sequence 14 AA;

Query Match      41.2%; Score 35; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 PPEIRTLTLE 12
   ||:|||||
Db 3 PPSLRITLLE 10

RESULT 5
AAW18869
ID AAW18869 standard; peptide; 14 AA.
XX
AC AAW18869;
XX
DT 05-JAN-1998 (first entry)
XX

```

```

XX 65 kD Glutamic acid decarboxylase peptide fragment 20.
DE
XX
KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
KW predisposition; autoimmune; tumour; rheumatoid arthritis;
KW multiple sclerosis.
XX
OS Synthetic.
XX
PN DE19526561-A1.
XX
PD 23-JAN-1997.
XX
PF 20-JUL-1995; 95DE-01026561.
XX
PR 20-JUL-1995; 95DE-01026561.
XX
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI Endl J, Ganz M, Stahl P, Kientsch-Engel R, Jung G, Pozzilli P;
PI Donie F;
XX
DR WPI; 1997-088254/09.
XX
PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
PT involving intradermal admin. of auto-reactive substances.
XX
PS Claim 11; Fig 2; 12pp; German.
XX
CC AAW18842-70 are peptide fragments of the 65 kD human glutamic acid
CC decarboxylase (GAD). The fragments are autoreactive substances used for
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
CC determined by using a claimed method for diagnosis of cell-mediated
CC diseases or a predisposition to cell-mediated diseases, which is effected
CC by administering an autoreactive substance intradermally and establishing
CC the diagnosis on the basis of the occurrence or lack of a positive
CC reaction at the site of administration. The method is used for diagnosis
CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM
XX
SQ Sequence 14 AA;

Query Match      41.2%; Score 35; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 PPEIRTLTLE 12
   ||:|||||
Db 3 PPSLRITLLE 10

RESULT 6
AAW12410
ID AAW12410 standard; peptide; 15 AA.
XX
AC AAW12410;
XX
DT 08-OCT-1997 (first entry)
XX
DE GAD65 residues 505-519.
XX
KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;
KW neuron; central nervous system; type 1 diabetes; autoimmune response;
KW T cell; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..15
FT /note= "optionally substituted, providing at least 7
FT residues remain wild type"
XX

```

PN WO9700891-A1.
 XX 09-JAN-1997.
 XX 24-JUN-1996; 96WO-US010790.
 XX 23-JUN-1995; 95US-00494624.
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PA (KENN-) KENNEDY INST RHEUMATOLOGY.
 PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.
 XX
 PI Londei M, Leslie RDG, Conlon PJ, Ling N, Gaur A;
 XX WPI; 1997-087322/08.
 XX New human glutamic acid decarboxylase peptide(s) - used for treatment,
 PT diagnosis and determining predisposition to diabetes and for ameliorating
 PT auto-immune responses.
 XX
 PS Claim 28; Page; 28pp; English.
 XX
 CC AA012403-W12413 represent fragments and analogues of the the 65 kD
 CC isoform of human glutamic acid decarboxylase (GAD65) (see AA012402 for
 CC full length wild type protein). GAD is an enzyme expressed in the beta
 CC cells of the pancreas, and in neurons of the central nervous system.
 CC There are two isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant
 CC regions of GAD65 have been identified in Type I diabetic patients. These
 CC GAD65 fragments, and analogues, are used in the methods of the invention.
 CC The methods are for detecting or treating diabetes or a predisposition to
 CC diabetes. The peptides can also be used for ameliorating an autoimmune
 CC response in a patient. Alteration of the native peptides with selective
 CC changes of crucial residues can induce unresponsiveness or change the
 CC responsiveness of antigen-specific autoreactive T cells. The peptide
 CC analogues compete for binding to MHC and do not cause proliferation of
 CC the corresponding native peptide-specific T cells
 XX
 SQ Sequence 15 AA;
 Query Match 41.2%; Score 35; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 5 PPSIRLTLE 12
 Db ||:||||
 6 PPSIRLTLE 13
 RESULT 7
 ID ADB88750 standard; peptide; 12 AA.
 XX
 AC ADB88750;
 DT 04-DEC-2003 (first entry)
 XX Payers patch and/or M cell specific targeting ligand peptide #19.
 XX Payer's patch cell; non-Payer's patch cell; transcription factor;
 KW upregulated protein; antigen; vaccine delivery; M cell; targeting ligand.
 XX Unidentified.
 OS
 XX WO2003004646-A2.
 XX 16-JAN-2003.
 XX 04-APR-2002; 2002WO-IB003866.
 XX 04-APR-2001; 2001US-0281387P.
 PR 02-JUL-2001; 2001US-0302591P.
 XX (OMAH/) O'MAHONY D J.

XX O'mahony DJ, Byrne D, Brayden D;
 XX WPI; 2003-229409/22.
 XX Increasing the levels of a protein in a Peyer's patch cell, useful for
 PT targeted vaccine or drug delivery, comprises delivering to the Peyer's
 PT patch cell a transcription factor or an activator of a transcription
 PT factor.
 XX
 PS Example 6; Page 50; 147pp; English.
 XX
 CC The invention relates to a novel method for increasing the levels of a
 CC protein in a Peyer's patch cell. The method comprises delivering to the
 CC cell a nucleic acid coding for a protein, the level of which or its mRNA
 CC is greater than in a non-Peyer's patch cell. The preferred protein of the
 CC invention is a transcription factor or a protein that activates a
 CC transcription factor selected from Jun-B, c-Jun related TF, Jun-B, STAT 3
 CC -signal transducer and activator of transcription 3, NkappaBgr; TF p105
 CC subunit, S-myc proto-oncogene, myc related, Nm23-M2, nucleoside
 CC diphosphate kinase B, metastasis reducing protein, and C-est-I proto-
 CC oncogene, and p54. The preferred upregulated protein of the invention is
 CC selected from clusterin, T-cell surface glycoprotein CD5 precursor, HSP
 CC 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a
 CC protein selected from the group. The method is useful for increasing or
 CC decreasing the level of a protein in a Peyer's patch cell, particularly
 CC in increasing antigen or vaccine delivery to M cells. The method may also
 CC be used to enhance transport of a drug through the gastrointestinal tract
 CC (GIT). This sequence represents a Payers patch and/or M cell specific
 CC targeting ligand peptide of the invention.
 XX
 SQ Sequence 12 AA;
 Query Match 40.0%; Score 34; DB 7; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WVSQPP 6
 Db |||||
 4 WASQPP 9
 RESULT 8
 ADC22832
 ID ADC22832 standard; peptide; 12 AA.
 XX
 AC ADC22832;
 XX
 DT 18-DEC-2003 (first entry)
 XX Intestinal epithelium targeting peptide, SEQ ID NO:19.
 DE Intestinal epithelial tissue; Peyer's patch; M-cell;
 XX gut-associated lymphoid tissue; Caco-2 cell; IEC-6 cell;
 KW homogenate membrane fraction; transcytosis; oral immunisation; vaccine;
 KW gene therapy; drug targeting; targeting peptide; ligand peptide.
 XX Synthetic.
 OS
 XX WO2003004517-A2.
 XX 16-JAN-2003.
 XX 28-JUN-2002; 2002WO-IB003401.
 XX 02-JUL-2001; 2001US-0302591P.
 PR (ELAN-) ELAN CORP PLC.
 XX O'mahony D, Lambkin I, Higgins L;
 PI WPI; 2003-275270/27.
 DR N-FSDB; ADC22886.

XX New Peyer's patch or M-cell targeting ligand, for facilitating the
 PT transport of e.g. drugs (such as, analgesics, insulin, antisease
 PT oligonucleotides or chemotherapy agents) or carriers through the human
 PT intestinal epithelium.
 XX
 PS Claim 1; SEQ ID NO 19; 91pp; English.
 XX
 CC The invention relates to synthetic peptides which are capable of binding
 CC to intestinal epithelial tissue, especially to Peyer's patch tissue
 CC and/or M-cells. The invention also encompasses nucleic acids encoding
 CC peptides of the invention. M-cells are antigen sampling cells that are
 CC found in the epithelium of the gut-associated lymphoid tissue, also known
 CC as Peyer's patch. Because the M-cells have transcytotic activity, which
 CC enables the downstream processing of the sampled antigen, the targeting
 CC of vaccines to M-cells should enhance oral immunisation. The peptides are
 CC also capable of binding to Caco-2 cells, IEC-6 cells, and rat, mouse, pig
 CC or dog homogenate membrane fractions. The peptides of the invention may
 CC be L-form, D-form, or retro-inverso peptides. The peptides of the
 CC invention are useful for targeting pharmaceutical agents (e.g., vaccines,
 CC genes, drugs, antigens or recombinant viruses) and carriers to the
 CC intestinal epithelial tissue of an organism, particularly a mammal. The
 CC ligands are also useful for facilitating the transport of such agents
 CC across the intestinal epithelium. The present sequence represents a
 CC specifically claimed peptide of the invention.
 XX
 SQ Sequence 12 AA;
 Query Match 40.0%; Score 34; DB 7; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WVSQPP 6
 | | | | |
 Db 4 WASQPP 9
 RESULT 9
 ADG17041
 ID ADG17041 standard; peptide; 15 AA.
 XX
 AC ADG17041;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human immunoglobulin E (IgE) P7 mimotope peptide SEQ ID NO:46.
 XX
 KW loop peptide; human; immunoglobulin E; IgE; mimotope; beta-lactam bond;
 KW immunogen; allergy; vaccine; antiallergic; IGE-antagonist; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WC2003092714-A2.
 XX
 PD 13-NOV-2003.
 XX
 PF 28-APR-2003; 2003WO-EP004551.
 XX
 PR 30-APR-2002; 2002GB-00009878.
 XX
 XX (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
 XX
 PI Vinals Y De BassolsC, Biemans R, Chomez LS;
 XX
 DR WPI; 2004-011821/01.
 XX
 XX New loop peptide from human IgE constrained by a beta-lactam bond, useful
 PT in the field of medicine, in particular for the manufacture of a
 PT medicament for the prevention and/or treatment of allergies.
 XX
 PS Claim 4; SEQ ID NO 46; 30pp; English.
 XX

CC The present invention describes a loop peptide (I) from human
 CC immunoglobulin E (IgE) of 5-20 amino acids, or their mimotopes,
 CC constrained by a beta-lactam bond. Also described: (1) a peptide having
 CC any of 36 fully defined sequences of 8-25 (SEQ ID NO:18-53) or their
 CC Mimotopes, where X is a methionine residue; (2) a mimotope in the peptide
 CC of (1); (3) an immunogen for the treatment of allergy, comprising a
 CC peptide of (1) or mimotope of (2), and optionally comprising a carrier
 CC molecule; (4) a vaccine comprising a peptide or mimotope or immunogen
 CC described above, optionally comprising an adjuvant; (5) a ligand which is
 CC capable of recognising the peptide of (1); (6) a pharmaceutical
 CC composition comprising the ligand of (5); (7) a method of manufacturing a
 CC vaccine, comprising the manufacture of an immunogen of (3), and
 CC formulating the immunogen with an excipient and/or adjuvant; (8) a method
 CC for treating a patient suffering or susceptible to allergy, comprising
 CC the administration of the vaccine of (4) or the pharmaceutical
 CC composition of (6) to the patient; (9) an isolated nucleic acid molecule
 CC encoding (1), the peptide of (1), the mimotope of (2) or the immunogen of
 CC (3); (10) an expression vector comprising the nucleic acid molecule of
 CC (9); and (11) a host cell comprising the expression vector of (10). (I)
 CC has anti-allergic activity, and can be used in vaccines, and as an IGE-
 CC antagonist. The methods and compositions of the present invention are
 CC useful for medicine, in particular for the manufacture of a medicament
 CC for the prevention and/or treatment of allergy. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 15 AA;
 Query Match 40.0%; Score 34; DB 8; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 2 VSQPPETRLGSC 15
 | | | | |
 Db 2 VTHPLRALDSC 15
 RESULT 10
 ABG67474
 ID ABG67474 standard; peptide; 9 AA.
 XX
 AC ABG67474;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human ADPI tryptic digest peptide #183.
 XX
 KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
 KW Alzheimer's disease-associated feature; neuroprotective;
 KW Alzheimer's disease-associated protein isoform; nootropic;
 KW ADPI tryptic digest peptide.
 XX
 OS Homo sapiens.
 OS
 XX
 FN WO200246767-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 29-NOV-2001; 2001WO-GB005289.
 XX
 PR 08-DEC-2000; 2000US-0254431P.
 XX
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 XX Herath HMAc, Parekh RB, Rohlf C;
 PI
 XX WPI; 2002-508575/54.
 DR
 XX
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprises detecting Alzheimer disease-associated features or Alzheimer
 PT disease-associated protein isoforms in brain tissue from the subject.
 XX
 PS Claim 7; Page 79; 427pp; English.
 XX

CC The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
 CC subject. The method comprises analysing a sample of brain tissue from a
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
 CC disease-associated features (ADFs), whose relative abundance correlates
 CC with the presence, absence, stage or severity of AD and comparing the
 CC abundance of each feature with the abundance of that chosen feature in
 CC brain tissue from persons free from AD. The invention also describes
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
 CC brain tissue. The methods and compositions of the invention are useful
 CC for the screening, diagnosis or prognosis of AD in a subject, for
 CC determining the stage or severity of AD in a subject, for identifying a
 CC subject at risk of developing AD, or for monitoring the effect of therapy
 CC administered to a subject having AD. Antibodies capable of binding to
 CC ADPIs are useful for treating or preventing AD, and for determining the
 CC efficacy of a given treatment regime. An agent that modulates the
 CC activity of ADPI is useful in the manufacture of a medicament for the
 CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
 CC human ADPI tryptic digest peptides
 CC
 CC Sequence 9 AA;

Query Match 38.8%; Score 33; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPPPE 7
 | : |||
 Db 2 WIPRPPE 8

RESULT 11
 ADA23585
 ID ADA23585 standard; peptide; 9 AA.
 AC ADA23585;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Alzheimer's disease-associated protein isoform tryptic peptide #194.
 DE human; Alzheimer's disease; vascular dementia; Lewy body dementia;
 KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
 KW Alzheimer's disease-associated protein isoform; ADPI.
 XX
 XX Homo sapiens.
 OS
 XX US2003064411-A1.
 PN
 XX 03-APR-2003.
 PD
 XX 10-DEC-2001; 2001US-00014340.
 PF
 XX 08-DEC-2000; 2000US-0254431P.
 PR
 XX (HERA/) HERATH H M A C.
 PA (PARE/) PAREKH R B.
 PA (ROHL/) ROHLFF C.
 XX
 XX Herath HMAC, Parekh RB, Rohlf C;
 PI
 XX WPI; 2003-540784/51.
 DR
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT involves analysing test sample of brain tissue from subject, and
 PT comparing feature in test sample with that of person(s) free from
 PT Alzheimer's disease.
 XX
 XX Disclosure; SEQ ID NO 194; 115pp; English.
 PS
 XX The invention relates to a method of screening or diagnosing Alzheimer's
 CC disease in a subject. The method is useful for screening, diagnosis or
 CC prognosis of Alzheimer's disease in a subject for determining the stage

CC of severity of Alzheimer's disease in a subject, for identifying a
 CC subject at risk of developing Alzheimer's disease, or for monitoring the
 CC effect of therapy administered to a subject having Alzheimer's disease.
 CC The method is also useful in treating vascular dementia, Lewy body
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
 CC depression. The inventive method identifies sensitive and specific
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
 CC It provides therapeutic agents for Alzheimer's disease that works
 CC quickly, potentially, specifically with fewer side effects. The present
 CC sequence represents the amino acid sequence of a Alzheimer's disease-
 CC associated protein isoform tryptic peptide.

XX Sequence 9 AA;

Query Match 38.8%; Score 33; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPPPE 7
 | : |||
 Db 2 WIPRPPE 8

RESULT 12
 AAR97328
 ID AAR97328 standard; peptide; 14 AA.
 XX
 AC AAR97328;

XX 15-OCT-1996 (first entry)
 XX
 XX Humanised monoclonal antibody heavy chain framework region.

XX Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
 KW complementary determining region; anti-carcinoembryonic antigen; CEA;
 KW diagnosis; imaging; therapy; immune response.
 XX
 XX Homo sapiens.

XX WO9611013-A1.
 PN
 XX 18-APR-1996.

XX 28-SEP-1995; 95WO-US011964.
 PF
 XX 05-OCT-1994; 94US-00318157.

XX (IMMU-) IMMUNOMEDICS INC.
 PA
 XX Hansen HJ, Armour KL;

XX WPI; 1996-209653/21.
 DR
 XX New humanised anti-CEA monoclonal antibody - having engrafted murine
 PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.

XX Claim 7; Page 39; 62pp; English.
 PS
 XX New humanised monoclonal antibodies (MAbs) comprising the complementary
 CC determining regions (CDRs) of a parental murine class III anti-
 CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
 CC heterologous antibody which can be derived from any species including
 CC human, retain the anti-CEA binding specificity of the parental MAb. The
 CC but are less immunogenic in a human subject than the parental MAb. The
 CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
 CC producing cancers and patients receiving the humanised antibodies and
 CC conjugates show improved therapeutic results, decreased immune responses
 CC and decreased immune-mediated adverse effects compared to the parent
 CC antibody. This sequence corresponds to the second framework region of the
 CC heavy chain of the humanised MAb. See AAR97313-97333

XX Sequence 14 AA;

Query Match 38.8%; Score 33; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
DB 1 WVRQPP 6

RESULT 13
AAU70479
ID AAU70479 standard; peptide; 14 AA.
XX
AC AAU70479;
XX
DT 14-FEB-2002 (first entry)
XX
DE Mouse heavy chain immunoglobulin framework region 2 #2.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Mus musculus.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
WPI; 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1B; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulfide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 14 AA;

Query Match 38.8%; Score 33; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
DB 1 WVRQPP 6

RESULT 15
ABJ18543
ID ABJ18543 standard; peptide; 14 AA.
XX
AC ABJ18543;

RESULT 14
AAU70495
ID AAU70495 standard; peptide; 14 AA.
XX
AC AAU70495;
XX
DT 14-FEB-2002 (first entry)
XX
DE Mouse heavy chain immunoglobulin framework region 2 #6.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Mus musculus.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
WPI; 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1B; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulfide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 14 AA;

Query Match 38.8%; Score 33; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
DB 1 WVRQPP 6

RESULT 15
ABJ18543
ID ABJ18543 standard; peptide; 14 AA.
XX
AC ABJ18543;

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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:48:28 ; Search time 139 Seconds
(without alignments)
38.182 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPPPIRTLEGSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 238011

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:
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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:
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18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:
19: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:
20: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	13 US-10-036-444-7	Sequence 7, Appli
2	38	44.7	14	10 US-09-791-551-80	Sequence 80, Appli
3	35	41.2	13	13 US-10-040-815-2	Sequence 2, Appli
4	35	41.2	13	13 US-10-040-815-5	Sequence 5, Appli
5	35	41.2	14	8 US-08-981-824-27	Sequence 27, Appli
6	34	40.0	12	14 US-10-185-815-19	Sequence 19, Appli
7	34	40.0	12	14 US-10-116-275-65	Sequence 65, Appli
8	33	38.8	9	14 US-10-014-340-193	Sequence 193, Appli
9	33	38.8	14	9 US-09-253-794-35	Sequence 35, Appli
10	33	38.8	14	9 US-09-730-857-99	Sequence 99, Appli
11	33	38.8	14	10 US-09-563-222-159	Sequence 159, Appli
12	33	38.8	14	10 US-09-563-222-175	Sequence 175, Appli
13	33	38.8	14	14 US-10-160-506-116	Sequence 116, Appli

14	33	38.8	14	14	US-10-428-662-108	Sequence 108, Appli
15	33	38.8	14	15	US-10-440-522-50	Sequence 50, Appli
16	33	38.8	14	16	US-10-449-379-116	Sequence 116, Appli
17	33	38.8	14	16	US-10-688-015-116	Sequence 116, Appli
18	33	38.8	14	16	US-10-327-598-26	Sequence 26, Appli
19	33	38.8	14	16	US-10-327-598-27	Sequence 27, Appli
20	33	38.8	14	17	US-10-783-950-148	Sequence 148, Appli
21	33	38.8	14	17	US-10-783-950-163	Sequence 163, Appli
22	33	38.8	14	17	US-10-160-505-116	Sequence 116, Appli
23	32	37.6	10	14	US-10-185-815-89	Sequence 89, Appli
24	32	37.6	14	9	US-09-855-271-30	Sequence 20, Appli
25	32	37.6	14	10	US-09-563-222-147	Sequence 147, Appli
26	32	37.6	14	10	US-09-563-222-187	Sequence 187, Appli
27	32	37.6	14	10	US-09-947-839-39	Sequence 39, Appli
28	32	37.6	14	10	US-09-791-551-82	Sequence 82, Appli
29	32	37.6	14	15	US-10-449-566-38	Sequence 38, Appli
30	32	37.6	14	15	US-10-440-522-62	Sequence 62, Appli
31	32	37.6	14	17	US-10-783-950-138	Sequence 138, Appli
32	32	37.6	14	17	US-10-783-950-174	Sequence 174, Appli
33	32	37.6	15	17	US-10-842-485-1	Sequence 1, Appli
34	32	37.6	15	17	US-10-842-485-3	Sequence 3, Appli
35	32	37.6	15	17	US-10-842-485-4	Sequence 4, Appli
36	32	37.6	15	17	US-10-842-485-5	Sequence 5, Appli
37	32	37.6	15	17	US-10-842-485-6	Sequence 6, Appli
38	32	37.6	15	17	US-10-842-485-7	Sequence 7, Appli
39	32	37.6	15	17	US-10-842-485-8	Sequence 8, Appli
40	32	37.6	15	17	US-10-842-485-12	Sequence 12, Appli
41	32	37.6	15	17	US-10-842-485-13	Sequence 13, Appli
42	32	37.6	15	17	US-10-842-485-16	Sequence 16, Appli
43	32	37.6	15	17	US-10-842-485-17	Sequence 17, Appli
44	32	37.6	15	17	US-10-842-485-18	Sequence 18, Appli
45	32	37.6	15	17	US-10-842-485-21	Sequence 21, Appli

ALIGNMENTS

RESULT 1

US-10-036-444-7
; Sequence 7, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1ei triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-FR-1060
; CURRENT APPLICATION NUMBER: US/10/036.444
; PRIOR FILING DATE: 2002-01-07
; PRIOR FILING DATE: 1999-11-15
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide derived
; OTHER INFORMATION: from natural sequence, useful for antiserum
; OTHER INFORMATION: production
US-10-036-444-7

Query Match 100.0%; Score 85; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVSQPPPIRTLEGSC 15

Db 1 WVSQPPPIRTLEGSC 15

RESULT 2
 US-09-791-551-80
 ; Sequence 80, Application US/09791551
 ; Publication No. US20030235594A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLOETZER, WILLIAM S.
 ; APPLICANT: HANNA, NABIL
 ; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
 ; FILE REFERENCE: 037003/0277869
 ; CURRENT APPLICATION NUMBER: US/09/791,551
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/185,390
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: 60/233,625
 ; PRIOR FILING DATE: 2000-09-18
 ; NUMBER OF SEQ ID NOS: 119
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 80
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-791-551-80

Query Match 44.7%; Score 38; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPP 6
 |||||
 DB 1 WVSQPP 6

RESULT 3
 US-10-040-815-2
 ; Sequence 2, Application US/10040815
 ; Publication No. US20020142004A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Leonard
 ; Honeyman, Margo
 ; Rudy, George
 ; Lew, Andrew
 ; TITLE OF INVENTION: IMMUNOREACTIVE AND IMMUNOTHERAPEUTIC
 ; MOLECULES
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/040,815
 ; FILING DATE: 07-Jan-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,272
 ; FILING DATE: 03-SEP-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; TELEPHONE: 516-742-4343
 ; TELEFAX: 516-742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-040-815-2

INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-040-815-2

Query Match 41.2%; Score 35; DB 13; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PPEIRLTLE 12
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 DB 5 PPSLRITLLE 12

RESULT 4
 US-10-040-815-5
 ; Sequence 5, Application US/10040815
 ; Publication No. US20020142004A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Leonard
 ; Honeyman, Margo
 ; Rudy, George
 ; Lew, Andrew
 ; TITLE OF INVENTION: IMMUNOREACTIVE AND IMMUNOTHERAPEUTIC
 ; MOLECULES
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/040,815
 ; FILING DATE: 07-Jan-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,272
 ; FILING DATE: 03-SEP-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; TELEPHONE: 516-742-4343
 ; TELEFAX: 516-742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-10-040-815-5

Query Match 41.2%; Score 35; DB 13; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PPEIRLTLE 12

Db 5 PPSLRLE 12
||.||||

RESULT 5
US-08-981-824-27
; Sequence 27, Application US/08981824
; Publication No. US20020114816A1
; GENERAL INFORMATION:
; APPLICANT: ENDL, Josef
; APPLICANT: STAHL, Peter
; APPLICANT: ALBERT, Winfried
; APPLICANT: SCHENDEL, Dolores
; APPLICANT: BOITARD, Christian
; APPLICANT: VAN ENDERT, Peter
; APPLICANT: JUNG, Gunther-Gerhard
; TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM HUMAN GLUTAMIC ACID
; TITLE OF INVENTION: DECARBOXYLASE (GAD)
; FILE REFERENCE: 564-7029
; CURRENT APPLICATION NUMBER: US/08/981,824
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: PCT/EP96/03093
; EARLIER FILING DATE: 1996-07-15
; EARLIER APPLICATION NUMBER: DE/195 25 784.7
; EARLIER FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-981-824-27

Query Match 41.2%; Score 35; DB 8; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PPSLRLE 12
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Db 3 PPSLRLE 10

RESULT 6
US-10-185-815-19
; Sequence 19, Application US/10185815
; Publication No. US20030096354A1
; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide ligand
US-10-185-815-19

Query Match 40.0%; Score 34; DB 14; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
| | | | |

Db 4 WASQPP 9

RESULT 7
US-10-116-275-65
; Sequence 65, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20057
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance U
US-10-116-275-65

Query Match 40.0%; Score 34; DB 14; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
| | | | |
Db 4 WASQPP 9

RESULT 8
US-10-014-340-193
; Sequence 193, Application US/10014340
; Publication No. US2003006411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Includin
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 193
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-193

Query Match 38.8%; Score 33; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 7
| | | | |
Db 2 WIPRPE 8

RESULT 9
US-09-253-794-35
; Sequence 35, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.

```

;
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
;
; INFORMATION FOR SEQ ID NO: 35:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-253-794-35

Query Match 38.8%; Score 33; DB 9; Length 14;
Best Local Similarity 83.3%; Pred. NO. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVSQPP 6
Db 1 WVRQPP 6

RESULT 10
US-09-730-857-99
; Sequence 99, Application US/09730857
; Patent No. US20020082396A1
;
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; Matsumoto, Yoshihiro
; Yamada, Yoshiki
; Sato, Koh
; Tsuchiya, Masayuki
; Yamazaki, Tatsumi
;
; TITLE OF INVENTION: Reshaped Human Antibody to
; Interleukin-8
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,857
; FILING DATE: 07-Dec-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 99:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-09-730-857-99

Query Match 38.8%; Score 33; DB 9; Length 14;
Best Local Similarity 83.3%; Pred. NO. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVSQPP 6
Db 1 WVRQPP 6

RESULT 11
US-09-563-222-159
; Sequence 159, Application US/09563222
; Publication No. US20030079253A1
;
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; Applicant: Hein, Mich B.
;
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; EUKARYOTIC CELLS
;
; FILE REFERENCE: 310098.406
;
; CURRENT APPLICATION NUMBER: US/09/563,222
;
; CURRENT FILING DATE: 2000-05-02
;
; NUMBER OF SEQ ID NOS: 197
;
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 159
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
;
; US-09-563-222-159

Query Match 38.8%; Score 33; DB 10; Length 14;
Best Local Similarity 83.3%; Pred. NO. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVSQPP 6
Db 1 WVRQPP 6

RESULT 12
US-09-563-222-175
; Sequence 175, Application US/09563222
; Publication No. US20030079253A1
;
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; Applicant: Hein, Mich B.
;
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN

```


; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-175

Query Match 38.8%; Score 33; DB 10; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
|||
Db 1 WVRQPP 6

RESULT 13
US-10-160-506-116
; Sequence 116, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-160-506-116

Query Match 38.8%; Score 33; DB 14; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
|||
Db 1 WVRQPP 6

RESULT 14
US-10-428-662-108
; Sequence 108, Application US/10428662
; Publication No. US20030185819A1
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Tempest, Philip R.
; TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
; FILE REFERENCE: 10274-007001
; CURRENT APPLICATION NUMBER: US/10/428,662
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US/08/454,899G
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/004,798
; PRIOR FILING DATE: 1993-01-12
; PRIOR APPLICATION NUMBER: PCT/US94/00266
; PRIOR FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heavy chain peptide
US-10-428-662-108

Query Match 38.8%; Score 33; DB 14; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
|||
Db 1 WVRQPP 6

RESULT 15
US-10-440-522-50
; Sequence 50, Application US/10440522
; Publication No. US20040091494A1
; GENERAL INFORMATION:
; APPLICANT: PIER, GERALD B.
; APPLICANT: PRESTON, MICHAEL J
; APPLICANT: CAVACINI, LISA
; APPLICANT: POSNER, MARSHALL
; TITLE OF INVENTION: P. AERUGINOSA MUCOID EXOPOLYSACCHARIDE SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: B00801.70285.US
; CURRENT APPLICATION NUMBER: US/10/440,522
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/153,437
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/292,365
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-522-50

Query Match 38.8%; Score 33; DB 15; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
|||
Db 1 WVRQPP 6

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Job time : 140 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:39:27 ; Search time 37 Seconds
(without alignments)
26.886 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPPEIRTLGSC 15

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	38.8	14	1	US-08-077-252B-15
2	33	38.8	14	1	US-08-137-117D-129
3	33	38.8	14	1	US-08-137-117D-129
4	33	38.8	14	2	US-08-436-717-134
5	33	38.8	14	2	US-08-436-717-134
6	33	38.8	14	2	US-08-318-157B-35
7	33	38.8	14	2	US-08-765-783A-99
8	33	38.8	14	3	US-09-002-753A-15
9	33	38.8	14	3	US-09-416-557-99
10	33	38.8	14	4	US-09-657-274-15
11	33	38.8	14	4	US-08-454-899G-108
12	33	38.8	14	4	US-09-253-794-35
13	33	38.8	14	4	US-09-563-222C-148
14	33	38.8	14	4	US-09-563-222C-163
15	32	37.6	14	1	US-08-077-252B-15
16	32	37.6	14	1	US-07-977-696C-39
17	32	37.6	14	1	US-08-129-930B-77
18	32	37.6	14	2	US-08-553-501A-77
19	32	37.6	14	2	US-08-553-501A-81
20	32	37.6	14	2	US-08-470-139-20
21	32	37.6	14	3	US-09-205-231-77
22	32	37.6	14	3	US-09-205-231-81
23	32	37.6	14	3	US-09-002-753A-16
24	32	37.6	14	3	US-08-134-346A-26
25	32	37.6	14	3	US-08-976-288A-39
26	32	37.6	14	3	US-09-347-061-20
27	32	37.6	14	4	US-09-657-274-16

Sequence 138, App
Sequence 174, App
Sequence 20, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 21, Appl

28 32 37.6 14 4 US-09-563-222C-138
29 32 37.6 14 4 US-09-563-222C-174
30 32 37.6 14 4 US-09-855-271-20
31 32 37.6 15 2 US-08-340-389A-1
32 32 37.6 15 3 US-08-245-712-1
33 32 37.6 15 4 US-09-508-054-1
34 32 37.6 15 4 US-09-508-054-3
35 32 37.6 15 4 US-09-508-054-4
36 32 37.6 15 4 US-09-508-054-5
37 32 37.6 15 4 US-09-508-054-6
38 32 37.6 15 4 US-09-508-054-7
39 32 37.6 15 4 US-09-508-054-8
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41 32 37.6 15 4 US-09-508-054-13
42 32 37.6 15 4 US-09-508-054-16
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44 32 37.6 15 4 US-09-508-054-18
45 32 37.6 15 4 US-09-508-054-21

ALIGNMENTS

RESULT 1

US-08-077-252B-15
; Sequence 15, Application US/08077252B
; Patent No. 5747854
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Lee, Byungkook
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Brinkmann, Ulrich
; TITLE OF INVENTION: Recombinant Disulfide-Stabilized
; TITLE OF INVENTION: Polypeptide Fragments Having Binding Specificity
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,252B
; FILING DATE: 14-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-152
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /label= FR2
; OTHER INFORMATION: /note= "Framework Region 2 (FR2) from
; OTHER INFORMATION: Monoclonal antibody McPC603 Heavy chain
; OTHER INFORMATION: variable region (V-H)"

US-08-077-252B-15

;; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;; NUMBER OF SEQUENCES: 158
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,717
;; FILING DATE: 19-FEB-1992
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/137,117
;; FILING DATE: 20-DEC-1993
;; APPLICATION NUMBER: WO PCT/JP92/00544
;; FILING DATE: 24-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 4-32084
;; FILING DATE: 19-FEB-1992
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 3-95476
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 129:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-436-717-129
Query Match 38.8%; Score 33; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WVSQPP 6
DB 1 WVRQPP 6
RESULT 5
US-08-436-717-134
; Sequence 134, Application US/08436717
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.

;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,717
;; FILING DATE: 19-FEB-1992
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/137,117
;; FILING DATE: 20-DEC-1993
;; APPLICATION NUMBER: WO PCT/JP92/00544
;; FILING DATE: 24-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 4-32084
;; FILING DATE: 19-FEB-1992
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 3-95476
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-436-717-134
Query Match 38.8%; Score 33; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WVSQPP 6
DB 1 WVRQPP 6
RESULT 6
US-08-318-157B-35
; Sequence 35, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424

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; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-157B-35

Query Match 38.8%; Score 33; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
Db 1 WVRQPP 6

RESULT 7
US-08-765-783A-99
; Sequence 99, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Teuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US/08/765,783A
; CLASSIFICATION: S30
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-765-783A-99
Query Match 38.8%; Score 33; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
Db 1 WVRQPP 6

RESULT 8
US-09-002-753A-15
; Sequence 15, Application US/09002753A
; Patent No. 6147203
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Lee, Byungkook
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Brinkmann, Ulrich
; TITLE OF INVENTION: Recombinant Disulfide-Stabilized
; TITLE OF INVENTION: Polypeptide Fragments Having Binding Specificity
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,753A
; FILING DATE: 05-JAN-1998
; CLASSIFICATION: S30
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,252
; FILING DATE: 14-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-152100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /label=PR2
; OTHER INFORMATION: /note="Framework Region 2 (FR2) from
; OTHER INFORMATION: Monoclonal antibody McPC603 Heavy chain
; OTHER INFORMATION: variable region (V-H)"
US-09-002-753A-15

Query Match 38.8%; Score 33; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
Db 1 WVRQPP 6
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OTHER INFORMATION: heavy chain peptide
US-08-454-899G-108

Query Match 38.8%; Score 33; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
|||
DB 1 WVRQPP 6

RESULT 12

US-09-253-794-35
; Sequence 35, Application US/09253794
; Patent No. 6676924

GENERAL INFORMATION:

APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 58
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-09-253-794-35
Query Match 38.8%; Score 33; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
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DB 1 WVRQPP 6

RESULT 13

US-09-563-222C-148
; Sequence 148, Application US/09563222C
; Patent No. 6696620

GENERAL INFORMATION:

APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 088904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 148
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-148

Query Match 38.8%; Score 33; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
|||
DB 1 WVRQPP 6

RESULT 14

US-09-563-222C-163
; Sequence 163, Application US/09563222C
; Patent No. 6696620

GENERAL INFORMATION:

APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 088904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 163
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-163

Query Match 38.8%; Score 33; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVSQPP 6
|||
DB 1 WVRQPP 6

RESULT 15

US-08-077-252B-16
; Sequence 16, Application US/08077252B
; Patent No. 5747654

GENERAL INFORMATION:

APPLICANT: Pastan, Ixa
; APPLICANT: Lee, Byungkook
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Brinkmann, Ulrich
; TITLE OF INVENTION: Recombinant disulfide-stabilized
; TITLE OF INVENTION: Polypeptide Fragments Having Binding Specificity
; NUMBER OF SEQUENCES: 23


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,252B
FILING DATE: 14-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..14
OTHER INFORMATION: /label= FR2
OTHER INFORMATION: /note= "Framework Region 2 (FR2) from
OTHER INFORMATION: Monoclonal antibody B3 Heavy chain
OTHER INFORMATION: variable region (V-H)"
US-08-077-252B-16

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Query Match      37.6%; Score 32; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVSQPPEIR 9
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Db 1 WVRQTPEKR 9

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Search completed: November 16, 2004, 19:52:19
Job time : 36 secs

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